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(54) Title: INTERMEDIATES AND ENZYMES OF THE NON-MEVALONATE ISOPRENOID PATHWAY

(57) Abstract: The invention provides a protein in a form that is functional for the enzymatic conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate notably in its (E)-form of the non-mevalonate biosynthetic pathway to isoprenoids. The invention also provides a protein in a form that is functional for the enzymatic conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its (E)-form, to isopentenyl diphosphate and/or dimethylallyl diphosphate. Further, screening methods for inhibitors of these proteins are provided. Further, 1-hydroxy-2-methyl-2-butenyl 4-diphosphate is provided and chemical and enzymatic methods of its preparation.

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Intermediates and enzymes of the non-mevalonate isoprenoid pathway

Field of the invention

The present invention relates to cells, cell cultures or organisms or parts thereof for the efficient formation of a biosynthetic product or intermediate or enzyme of a 1-deoxy-D-xylulose 5-phosphate-dependent biosynthetic pathway. Further, the invention relates to vectors for producing them. Further, the invention relates to their use for the formation or production of intermediates or products or enzymes of said biosynthetic pathway as well as to enzymes and intermediates. Further, the invention relates to the screening for inhibitors or enzymes for said biosynthetic pathway.

Background of the invention

The system of biosynthetic pathways in any organism is highly streamlined, whereby a few central trunk pathways branch into a great number of peripheral pathways. The central trunk pathways involve starting materials which are highly integrated. Therefore, central or trunk pathways are highly regulated. At the same time they are crucial for any attempts to interfere with the metabolism of any organism either by an inhibitor or by metabolic engineering.

The isoprenoid pathways are a prime example for this metabolic organisation. They are very long and highly branched, leading to some 30,000 isoprenoid or terpenoid compounds. They all seem to derive from isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP). They are produced by two alternative trunk pathways (reviewed in Eisenreich et al., 2001).

By the classical research of Bloch, Cornforth, Lynen and co-workers, isopentenyl pyrophosphate (IPP) and dimethylallyl pyrophosphate (DMAPP) have become established as key intermediates in the biosynthesis of isoprenoids via mevalonate. However, many bacteria, plastids of all plants, and the protozoon *Plasmodium falciparum* synthesize IPP and DMAPP by an alternative pathway via 1-deoxy-D-xylulose 5-phosphate. The discovery of the pathway was mainly based on the incorporation of isotope-labelled 1-deoxy-D-xylulose into the isoprenoid side chain of menaquinones from *Escherichia coli* (Arigoni and Schwarz, 1999).

This mevalonate-independent pathway has so far only been partially explored (Fig. 1). For a better understanding of these aspects of the invention, the pathway shall be briefly explained. It can be divided into three segments:

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In a first pathway segment shown in Fig. 1, pyruvate (1) is condensed with glyceraldehyde 3-phosphate (2) to 1-deoxy-D-xylulose 5-phosphate (DXP) (3). Subsequently, DXP is converted into 2C-methyl-D-erythritol 4-phosphate (MEP) (4) by a two-step reaction comprising a rearrangement and a reduction. This establishes the 5-carbon isoprenoid skeleton.

In the subsequent segment of the mevalonate-independent pathway (Fig. 1), MEP (4) is first condensed with CTP to 4-diphosphocytidyl-2C-methyl-D-erythritol (CDP-ME) (5) by 4-diphosphocytidyl-2C-methyl-D-erythritol synthase (PCT/EP00/07548). CDP-ME (5) is subsequently ATP-dependent phosphorylated by 4-diphosphocytidyl-2C-methyl-D-erythritol kinase yielding 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate (CDP-MEP) (6). The intermediate is subsequently converted into 2C-methyl-D-erythritol 2,4-cyclodiphosphate (cMEPP) (7) by 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (PCT/EP00/07548). These three enzymatic steps form a biosynthetic unit which activates the isoprenoid C₅-skeleton for the third pathway segment (Rohdich *et al.*, 1999; Lüttgen *et al.*, 2000; Herz *et al.*, 2000).

Bioinformatic studies (German Patent Application 10027821.3), as well as studies with mutants of *Synechocystis* sp. (Cunningham *et al.*, 2000) and *Escherichia coli* (Campos *et al.*, 2001; Altincicek *et al.*, 2001) demonstrate the involvement of *lytB* and *gcpE* genes in the isoprenoid pathway. However, the function and the reaction catalyzed by the corresponding gene products are still unknown.

Recently, a kinase (XylB) has been described that catalyzes the conversion of 1-deoxy-D-xylulose into 1-deoxy-D-xylulose 5-phosphate at high rates (Wungsintaweekul *et al.*, 2000). Genes and enzymes participating in further downstream reactions have been described. However, the gene functions, the intermediates, and the mechanisms leading to the products are still unknown.

For numerous pathogenic eubacteria as well as for the malaria parasite *P. falciparum*, the enzymes involved in the non-mevalonate pathway are essential. The intermediates of the mevalonate-independent pathway cannot be assimilated from the environment by pathogenic eubacteria and *P. falciparum*. The enzymes of the alternative isoprenoid pathway do not occur in mammalia which synthesize their isoprenoids and terpenoids exclusively via the mevalonate pathway. Moreover, the idiosyncratic nature of the reactions in this pathway reduces the risk of cross-inhibitions with other, notably mammalian enzymes.

Therefore, enzymes of the alternative isoprenoid pathway seem to be specially suited as

targets for novel agents against pathogenic microorganisms and herbicides. The elucidation of unknown steps and the identification of these targets, e.g. genes and cognate enzymes of these pathways is obligatory for this purpose.

A further source of interest in the non-mevalonate pathway derives from the fact certain pathogens like *Mycobacteria*, *Plasmodia*, *Escherichia* etc. use this pathway to activate $\gamma\delta$ T cells (Fournié and Bonneville, 1996). Therefore, $\gamma\delta$ T cells likely act as a first line of defense against infections by such pathogens. Intermediates of the non-mevalonate pathway have been suggested to be responsible for $\gamma\delta$ T cell activation (Jomaa *et al.*, 1999). Recently, it was shown that *E. coli* strains lost the ability to stimulate $\gamma\delta$ T cells when the *dxr* or the *gcpE* gene was knocked out (Altincicek *et al.*, 2001).

Moreover, there is a great biotechnological interest in these pathways, since they lead to valuable vitamins and isoprenoid or terpenoid products.

Previous attempts to approach these goals have been hampered by the low rate of biosynthesis along these pathways in wild-type cells studied so far.

Summary of the invention

It is an object of the invention to provide enzymes and nucleic acids coding for said enzymes as well as intermediates for the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to isopentenyl diphosphate and/or dimethylallyl diphosphate.

It has surprisingly been found that the intermediate in the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to isopentenyl diphosphate and/or dimethylallyl diphosphate is 1-hydroxy-2-methyl-2-butenyl 4-diphosphate. This intermediate is formed by an enzyme encoded by *gcpE* as designated in the *E. coli* genome. It has further been found that this enzyme prefers as reductant NADH or NADPH. Further, it has been found that it is promoted by Co^{2+} .

The above intermediate is converted to isopentenyl diphosphate and/or dimethylallyl diphosphate by an enzyme encoded by *lytB* as designated in the *E. coli* genome. The latter enzyme prefers as reductant NADH or NADPH and FAD as mediator. Further it can be promoted by ions of a metal selected from manganese, iron, cobalt, nickel.

With these findings, the third segment of the trunk non-mevalonate pathway is now

established. The key to these findings is the intermediate 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its *E*-form. This establishes the unifying principle of the invention for reactions to and from this intermediate.

Further, it is an object of the invention to provide cells, cell cultures, organisms or parts thereof for the efficient biosynthesis of isoprenoid products or intermediates of the non-mevalonate biosynthetic pathway dependent on 1-deoxy-D-xylulose 5-phosphate production from 1-deoxy-D-xylulose and/or glucose.

The present invention produces a novel *in vivo* system which can be used for the structure elucidation of unknown intermediates and the assignment of biological functions of putative genes or cognate enzymes in the alternative isoprenoid biosynthetic pathway. As an example, the functional assignment of the *gcpE* gene (now designated as *ispG*) and of the *lytB* gene (now designated *ispH*) in the mevalonate-independent pathway of isoprenoid biosynthesis is achieved.

More specifically, said *in vivo* system consists of recombinant *E. coli* strains harbouring vector construct(s) carrying and expressing genes for D-xylulokinase (*xylB*), and genes of further downstream steps of terpenoid biosynthesis, such as *dxs*, *dxr*, and/or *ispD*, and/or *ispE*, and/or *ispF*, and/or *gcpE*, and/or *lytB* from *E. coli*, and/or a carotenoid gene cluster from *Erwinia uredovora*.

In one aspect of the invention, the genetically modified strains can be fed with 1-deoxy-D-xylulose, notably with isotope-labelled 1-deoxy-D-xylulose, which is converted at high rates into the common intermediate of the mevalonate-independent terpenoid pathway, 1-deoxy-D-xylulose 5-phosphate, and into further intermediates of said pathway, like 2C-methyl-D-erythritol 4-phosphate, 4-diphosphocytidyl-2C-methyl-D-erythritol, 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate, 2C-methyl-D-erythritol 2,4-cyclodiphosphate, 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, isopentenyl diphosphate, and dimethylallyl diphosphate. Further, feeding with glucose or an intermediate of glycolysis for conversion into said further intermediates of said pathway may be performed.

Said systems are useful for the structure elucidation of hitherto elusive intermediates in the

biosynthetic pathways, for *in vivo* screening of novel antibiotics, antimalarials, and herbicides, and as a platform for the bioconversion of exogenous 1-deoxy-D-xylulose and/or glucose into intermediates and products of the non-mevalonate pathway of terpenoid biosynthesis.

Said systems can also be used for screening chemical libraries for potential herbicides, and/or antimalarials, and/or antimicrobial substances by detecting and measuring the amount of certain intermediates formed *in vivo* in the presence or absence of potential inhibitors of the gene products of mevalonate-independent isoprenoid pathway genes, namely *dxs*, *dxr*, *ispD*, *ispE*, *ispF*, *gcpE*, and *lytB*.

Said system can further be used for the production of higher isoprenoids (e.g. isoprenoids having 10, 15, 20, 30 or 40 carbon atoms) such as carotene, α -tocopherole or vitamins by boosting the bioynthesis of isopentenyl diphosphate and/or dimethylallyl diphosphate via the non-mevalonate pathway, e.g. by using glucose as feeding material. Further feeding materials which may be used are intermediates or products of glycolysis like glyceraldehyde 3-phosphate or pyruvate.

Further, this invention provides novel compounds of formula I (see below), notably 1-hydroxy-2-methyl-2-butenyl 4-diphosphate as well as enzymatic and chemical methods for preparing said compounds. As demonstrated herein, (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate is produced from 2C-methyl-D-erythritol 2,4-cyclodiphosphate by the *gcpE* gene product.

It is further demonstrated herein that (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate is converted to dimethylallyl diphosphate and isopentenyl diphosphate by the *lytB* gene product.

Short description of the figures and annexes

Figure 1: Biosynthesis of both isoprenoid precursors, isopentenyl pyrophosphate and dimethylallyl pyrophosphate via the mevalonate-independent pathway.

Figure 2: Scheme of an *Escherichia coli* *in vivo* system for generating optionally isotopically labelled intermediates of biosynthetic pathways such as the mevalonate-independent isoprenoid biosynthesis, and for the production of higher terpenoids such as carotenoids.

Figure 3: ¹H NMR spectra in D₂O (pH 6) obtained according to Example 25. * indicates impurities.

Figure 4: Preparation of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate according to Example 24. Reagents and conditions were as follows: (a) DHP, PPTS, 25 °C (2.5 h); (b) Ph₃PCHCO₂Et, toluene, reflux (39 h); (c) (1) DIBALH, CH₂Cl₂, -78 °C (3 h), (2) 1 M NaOH/H₂O; (d) p-TsCl, DMAP, CH₂Cl₂, 25 °C (1 h); (e) ((CH₃CH₂CH₂CH₂)₄N)₃HP₂O₇, MeCN, 25 °C (2 h); (f), HCl/H₂O pH 1, 25 °C (7 min).

Figure 5: The reaction catalyzed by the *ispH* (formerly *lytB*) gene product.

Figure 6: The reaction catalyzed by the *ispG* (formerly *gcpE*) gene product.

Figure 7: Chemical preparation of 3-formyl-but-2-enyl 1-diphosphate (see example 42).

Annex A: DNA sequence of the vector construct pBSxylBdxr.

Annex B: DNA sequence of the vector construct pBSxylBdxrispD.

Annex C: DNA sequence of the vector construct pBS_{cyclo}.

Annex D: DNA sequence of the vector construct pACYCgcpE.

Annex E: DNA sequence of the vector construct pBScaro14.

Annex F: DNA sequence of the vector construct pACYCcaro14.

Annex G: DNA sequence and corresponding amino acid sequence of the *ispG* (formerly *gcpE*) gene from *Escherichia coli*.

Annex H: DNA sequence of the vector construct pBS_{cyclogcpE}.

Annex I: DNA sequence of the vector construct pACYClytBgcpE.

Annex J: DNA and corresponding amino acid sequence of the *ispH* (formerly *lytB*) gene from *Escherichia coli*.

Annex K: DNA sequence of the vector construct pBS_{cyclogcpE}lytB2.

Annex L: DNA and corresponding amino acid sequence of the *ispG* gene (fragment) from *Arabidopsis thaliana*.

Annex M: DNA and corresponding amino acid sequence of the *ispG* (formerly *gcpE*) gene of *Arabidopsis thaliana*.

Annex N: cDNA sequence of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (Isph) from *Arabidopsis thaliana*

Detailed description of the invention

1-Deoxy-D-xylulose 5-phosphate is a common intermediate in the alternative terpenoid pathway via 2C-methyl-D-erythritol 4-phosphate. This latter pathway is operative in bacteria, certain protozoa and most significantly also in the plastids of plants, where it is in charge of the biosynthesis of a great many valuable terpenoid products, like natural rubber, carotenoids, menthol, menthone, camphor or paclitaxel. The alternative terpenoid pathway is now intensely studied. But so far only the initial steps from glyceraldehyde 3-phosphate and pyruvate via 1-deoxy-D-xylulose 5-phosphate and 2C-methyl-D-erythritol 4-phosphate, 4-diphosphocytidyl-2C-methyl-D-erythritol, 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate and 2C-methyl-D-erythritol 2,4-cyclodiphosphate (Fig. 1) have been elucidated.

The intermediate 1-deoxy-D-xylulose 5-phosphate is of most crucial significance for a number of commercial purposes:

- (1) It may be used as a key intermediate for commercial screening procedures regarding potential inhibitors of downstream enzymes in the biosynthesis of the alternative terpenoid pathway.
- (2) It may be used as a key intermediate for the *in vitro* production of terpenoids or of intermediates thereof.
- (3) It occurs *in vivo* in the biosynthesis of terpenoids as an enzymatic condensation product of glyceraldehyde 3-phosphate and pyruvate. The latter are central intermediates of the metabolism and obligatory starting materials for numerous biosynthetic pathways. Therefore, it is desirable to generate a high level of 1-deoxy-D-xylulose 5-phosphate *in vivo* from an exogenous source and thus independent from the pools of glyceraldehyde 3-phosphate and pyruvate for boosting the biosynthesis of terpenoids or of intermediates thereof in microorganisms or cell cultures that are either naturally or recombinantly endowed with the pathway of interest without influencing the basic intermediary metabolism of the cells.
- (4) 1-Deoxy-D-xylulose 5-phosphate can be generated from 1-deoxy-D-xylulose by the catalytic action of the *xyfB* gene product. Using recombinant strains comprising the *xyfB* gene the reaction occurs *in vivo* and exogenous 1-deoxy-D-xylulose is converted into intracellular 1-deoxy-D-xylulose 5-phosphate at high rates.
- (5) 1-DXP can be generated from glucose by the catalytic action of glycolytic enzymes and DXP-synthase. Using recombinant strains comprising the *dxs* gene, the reaction occurs *in vivo* and exogenous glucose is converted to intracellular 1-DXP at high rates.

It is an aspect of the invention to use 1-deoxy-D-xylulose as a precursor in order to boost the rates of biosynthesis of 1-deoxy-D-xylulose 5-phosphate-dependent pathways. 1-Deoxy-D-xylulose can be prepared by various published procedures (Blagg and Poulter, 1999; Kennedy et al., 1995; Piel and Boland, 1997; Shono et al., 1983; Giner, 1998).

It is an aspect of the present invention to use 1-deoxy-D-xylulose in various isotopically labelled forms. It may be labelled by radioactive isotopes or non-radioactive isotopes of C (^{13}C or ^{14}C), H (D or T) or O (^{17}O or ^{18}O) in any combination.

Isotope-labelled 1-deoxy-D-xylulose may be prepared enzymatically using 1-deoxy-D-xylulose 5-phosphate synthase of *Bacillus subtilis* and commercially available glycolytic enzymes and phosphatase from isotope-labelled glucose and/or pyruvate (PCT/EP00/07548).

1-Deoxy-D-xylulose may be used as a free acid or as a salt, preferably as an alkaline (e. g., lithium, sodium, potassium) salt or as an ammonium or amine salt.

It is an aspect of the present invention to use recombinant cells, cell cultures, or organisms or parts thereof for the formation of biosynthetic products or intermediates or enzymes or for the screening for antimicrobials, antimalarials or herbicides.

For carrying out the present invention various techniques in molecular biology, microbiology and recombinant DNA technology are used which are comprehensively described in Sambrook et al., Molecular Cloning, second edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York; in DNA Cloning: A Practical Approach, Vol. 1 and 2, 1985 (D. N. Glover, ed.); in Oligonucleotide Synthesis, 1984 (M. L. Gait, ed.); and in Transcription and Translation (Hames and Higgins, eds.).

Nucleic acids

The present invention comprises nucleic acids which include prokaryotic, protozoal and plant sequences and derived sequences. A derived sequence relates to a nucleic acid sequence corresponding to a region of the sequence or orthologs thereof or complementary to "sequence-conservative" or "function-conservative" variants thereof.

Sequences may be isolated by well known techniques or are commercially available (Clontech, Palo Alto, CA; Stratagene, LaJolla, CA). Alternatively, PCR-based methods can be used for

amplifying related sequence from cDNA or genomic DNA.

The nucleic acids of the present invention comprise purine and pyrimidine containing polymers in various amounts, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribonucleotides. The nucleic acids may be isolated directly from cells. Alternatively, PCR may be used for the preparation of the nucleic acids by use of chemical synthesized strands or by genomic material as template. The primers used in PCR may be synthesized by using the sequence information provided by the present invention or from the database and additionally may be constructed with optionally new restriction sites in order to ease the cloning in a vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural regulation sequences or may be associated with heterologous sequences, including promoter, enhancer, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3' noncoding regions or similar. The nucleic acids may be modified on basis of well known methods. Non-limiting examples for these modifications are methylations, "Caps", substitution of one or more natural nucleotides with an analogue, and internucleotide modification, i.e. those with uncharged bond (i.e. methylphosphonates, phosphotriester, phosphoramidates, carbamates, etc.) and with charged bond (i.e. phosphorothiacates, etc.). Nucleic acids may carry additional covalent bound units such as proteins (i.e. nucleases, toxins, antibodies, signalpeptides, poly-L-lysine, etc.), intercalators (i.e. acridine, psoralene, etc.), chelators (i.e. metals, radioactive metals, iron, oxidative metals, etc.) and alkylators. The nucleic acids may be derived by formation of a methyl- or ethylphosphotriester bond or of a alkylphosphoramidate bond. Further, the nucleic acids of the present invention may be modified by labeling, which give an either directly or indirectly detectable signal. Examples for these labeling include radioisotopes, fluorescent molecules, biotin and so on.

Vectors

The invention provides nucleic acid vectors, which comprise the sequences provided by the present invention or derivatives thereof. Various vectors, including plasmids or vectors for fungi have been described for the replication and/or expression in various eucaryotic and procaryotic hosts. High copy replication vectors are preferred for the purposes of the invention. Non-limiting examples include pKK plasmids (Clontech), pUC plasmids (Invitrogen, San Diego, CA), pET plasmids (Novagen, Inc., Madison, WI) or pRSET or pREP (Invitrogen) and various suitable host cells on basis of well known techniques. Recombinant cloning vectors comprise

often more than one replication system for the cloning and expression, one or more marker for the selection in the host; i.e. antibiotic resistance and one or more expression cartridge. Suitable hosts may be transformed/transfected/infected by a method as suitable including electroporation, CaCl_2 -mediated DNA incorporation, tungae infection, microinjection, microbombardment or other established methods.

Suitable hosts include bacteria, archaeobacteriae, fungi, notable yeast, plants, notably *Arabidopsis thaliana*, *Mentha piperita* or *Taxus sp.* and animal cells, notably mammalian cells. Most important are *E. coli*, *Bacillus subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells and immortalized myeloid and lymphoid mammalian cells. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus and so on. A great number of transcription, initiation (including ribosomal binding sites) and termination regulation regions have been isolated and there efficiency for the transcription and translation of heterologous proteins has been demonstrated in various hosts. Examples for these regions, methods for the isolation, the way for using are well known. Under suitable conditions for expression host cells may be used as source for the recombinant synthesized proteins.

Expression systems

Preferable vectors may include a transcription element (that is a promoter), functionally connected with the enzyme domain. Optionally, the promoter may include parts of operator region and/or ribosomal binding sites. Non-limiting examples for bacterial promoters, which are compatible with *E. coli*, include: *trc* promoter, β -lactamase (penicillinase) promoter; lactose promoter, tryptophan (*trp*) promoter, arabinose BAD operon-promoter, lambda-derived P1 promoter and N gene ribosomal binding site and the hybrid Tac promoter, derived from sequences of *trp* and *lac* UV5 promoters. Non-limiting examples for yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde 3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactoeprimase promoter and alcoholdehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limiting viral promoters such as i.e. simian virus 40 (SV40), rous sarcoma virus (RSV), adenovirus (ADV) and bovine papilloma virus (BPV). Mammalian cells may also need terminator sequences and poly-A sequences and enhancer sequences, which may increase the expression. Sequences, which amplify the genes, may also be preferred. Further on,

sequences may be included, which ease the secretion of the recombinant protein from the cell, which may be but non-limiting a bacterial, yeast or animal cell, such as i.e. a secretion signal sequence and/or prehormon sequence.

It is an important aspect of the invention that the combined recombinant endowment with *xyIB* and other gene(s) of the alternative C5-isoprenoid pathway and optionally gene(s) for higher isoprenoids or terpenoids boost(s) these pathways. Preferably, *xyIB* is combined with complete sets of genes to convert 1-deoxy-D-xylulose 5-phosphate into the desired intermediate or end products. For intermediates in the C5-isoprenoid pathway, cells are preferably endowed with one of the combinations of genes given in claim 76.

For the genes cited herein, the common *E. coli* designation were used. Other genes from *E. coli* or from other organisms (orthologous genes) may also be used if they have the same functions (function-conservative genes), notably if their gene products catalyze the same reaction. Further, deletion or insertion variants or fusions of these genes with other genes or nucleic acids may be used, as long as these variants are function-conservative. The above genes may be derived from bacteria, protozoa, or from higher or lower plants,

It is another important aspect of the invention that the function of *gcpE* as following immediately downstream from *ispF* has been determined. Our findings show that the *gcpE* gene product is involved in the formation of the novel compound 1-hydroxy-2-methyl-2-butenyl 4-diphosphate from 2C-methyl-D-erythritol 2,4-cyclodiphosphate. Therefore, we rename *gcpE* in *ispG*.

In a further aspect of the invention it was shown that the gene product of *gcpE* is involved in the formation of the *E*-isomer of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate from 2C-methyl-D-erythritol 2,4-cyclodiphosphate by comparison with chemically synthesized (*E*)- and (*Z*)-isomers of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate. Therefore, this invention further pertains to the (*E*) and (*Z*) isomers of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate salts or protonated forms thereof.

It is another important aspect of the invention that the function of *lytB* has been determined as following immediately downstream from *ispG*. Therefore, it is renamed *ispH*. It is our finding

that *ispH* is involved in the conversion of (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate into isopentenyl 4-diphosphate and/or dimethylallyl 4-diphosphate.

It should be understood that „1-hydroxy-2-methyl-2-butenyl 4-phosphate" and „1-hydroxy-2-methyl-2-butenyl 4-diphosphate" comprise the free phosphoric and diphosphoric acids, respectively, and the singly or multiply deprotonated forms thereof, i.e. salts which may be salts of any cation (including Na, K, NH₄⁺, Li, Mg, Ca, Zn, Mn, and Co cations). The protonation state of (di)phosphates and phosphate derivatives or their conjugated acids in aqueous solution depends on the pH value of the solution, as is known to persons skilled in the art. The same applies to other phosphates or phosphate derivatives.

In another aspect of the invention, (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate has been successfully incorporated into the lipid soluble fraction of *Capsicum annuum* chromoplasts. A ¹⁴C label of this compound was incorporated into the geranylgeraniol, β-carotene, phytoene and phytofluene fractions of *C. annuum* chromoplasts establishing (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate as intermediate of the non-mevalonate pathway downstream from 2C-methyl-D-erythritol 2,4-cyclodiphosphate and upstream from isopentenyl diphosphate.

It is another aspect of the invention that *xyfB* can be combined with *gcpE* and optionally other genes of the alternative C5 isoprenoid pathway and/or of the higher isoprenoid pathways in vector(s) for recombinant engineering.

As a consequence of our findings regarding *gcpE* (now *ispG*) it follows that the gene *lytB* operates downstream of *gcpE* and thus in service of the conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate to IPP and/or DMAPP. Therefore, it is another aspect of the invention to combine the gene *lytB* with *xyfB* and optionally other genes of the common C5-isoprenoid pathway or of a higher isoprenoid pathway.

Our finding allows the efficient formation or production of intermediates or products of the isoprenoid pathway with any desired labelling, notably the following intermediates:

2C-methyl-D-erythritol 4-phosphate; 4-diphosphocytidyl-2C-methyl-D-erythritol; 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate; 2C-methyl-D-erythritol 2,4-

cyclodiphosphate; 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, isopentenyl diphosphate; dimethylallyl diphosphate.

The formation of end products of the terpenoid pathway (e. g., β -carotene, zeaxanthine, paclitaxel, menthol, menthone, cannabinoids), may be boosted following the process of the invention.

The strains harbouring the recombinant plasmids can be cultivated in conventional culture media, preferably in terrific broth medium, at 15 to 40 °C. The preferred temperature is 37 °C. The *E. coli* strains are induced with 0.5 to 2 mM isopropyl- β -D-thiogalactoside (IPTG) at an optical density at 600 nm from 0.5 to 5. The cells are incubated after addition of 1-deoxy-D-xylulose at a concentration of 0.001 mM to 1 M preferably at a concentration of 0.01 to 30 mM for 30 min to 15 h, preferably 1 to 5 h.

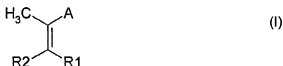
It has been found that the process of producing isoprenoid intermediates or products by the genetically engineered organisms of the invention can be boosted by supplying a source for CTP, for example cytidine and/or uridine and/or cytosine and/or uracil and/or ribose and/or ribose 5-phosphate and/or any biosynthetic precursors of CTP at a concentration of 0.01 to 10 mM, preferably at a concentration of 0.3 to 1 mM, and/or by supplying a source for phosphorylation activity, for example glycerol 3-phosphate and/or phosphoenolpyruvate and/or ribose 5-phosphate at a concentration of 0.1 to 100 mM, preferably at a concentration of 0.5 to 10 mM and/or inorganic phosphate and/or inorganic pyrophosphate at a concentration of 1 to 500 mM, preferably at a concentration of 10 to 100 mM and/or any organic phosphate and/or pyrophosphate, and/or by supplying a source for reduction equivalents, for example 0.1 to 1000 mM, preferably 10 to 1000 mM, lactate and/or succinate and/or glycerol and/or glucose and/or lipids at a concentration of 0.1 to 100 mM, preferably at a concentration of 0.5 to 10 mM. A particularly efficient production process is specified in claims 72 and 80 to 84.

This process can also be used with great advantages for screening for inhibitors of the enzymes involved or of downstream enzymes, dependent on the choice of the isoprenoid intermediate or product for detection. The enzymes *dxs*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG* (formerly *gcpE*) and *ispH* (formerly *lytB*) do not occur in animals. Therefore inhibitors against *dxs*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG* (formerly *gcpE*) and *ispH* (formerly *lytB*) have great value as (a) herbicides against weed plants or algae; (b) antibiotic agents against pathogenic bacteria; (c) agents against protozoa, like *Plasmodium falciparum*, the causative pathogen of malaria.

The activity of the said enzymes can be detected (in the presence or absence of a potential inhibitor) by measuring either the formation of a product or the consumption of an intermediate, preferably by TLC, HPLC or NMR.

With the finding that 1-hydroxy-2-methyl-2-butenyl 4-diphosphate is an intermediate of the non-mevalonate terpenoid pathway we have acquired essential determinants of the structure of inhibitors. Namely, the structures of a subset of inhibitors should be similar to at least a portion of the starting compound or the product or the transition state between the starting compound e.g. 2C-methyl-D-erythritol 2,4-cyclodiphosphate and the product e. g. 1-hydroxy-2-methyl-2-butenyl 4-diphosphate.

This invention discloses novel compounds, or salts thereof, of the following formula I:



whereby R^1 and R^2 are different from each other and one of R^1 and R^2 is hydrogen and the other is selected from the group consisting of $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$, $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})_2$, and $-\text{CH}_2\text{OH}$, and whereby A stands for $-\text{CH}_2\text{OH}$ or $-\text{CHO}$. These compounds may be isotope-labelled.

In formula I, A preferably stands for $-\text{CH}_2\text{OH}$.

Among R^1 and R^2 , R^1 is preferably hydrogen and R^2 is preferably selected from the group consisting of $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$ and $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})_2$.

In the group consisting of $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$ and $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})_2$, $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$ is preferred.

If a compound of formula I is a salt, it may e.g. be a lithium, sodium, potassium, magnesium, ammonium, manganese salt. These salts may derive from a single or from multiple deprotonations from the (di)phosphoric acid moiety.

The novel compounds disclosed herein are useful for various applications e.g. for screening for genes, enzymes or inhibitors of the biosynthesis of isoprenoids or terpenoids, either *in vitro* in the presence of an electron donor or *in vivo*.

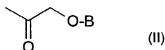
This invention further provides a process for the chemical preparation of a compound of

formula I or a salt thereof:



wherein A represents $-\text{CH}_2\text{OH}$ and R^1 and R^2 are different from each other and one of R^1 and R^2 is hydrogen and the other is $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$, $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})_2$ or $-\text{CH}_2-\text{OH}$ by the following steps:

- (a) converting a compound of the following formula (II):



wherein B is a protective group into a compound of the following formula (III) or (IV):



(III)



(IV)

by a Wittig or Horner reagent, wherein the group D is a precursor group convertible reductively to a $-\text{CH}_2-\text{OH}$ group;

- (b) reductively converting group D to a $-\text{CH}_2-\text{OH}$ group;
- (c) optionally converting group $-\text{CH}_2-\text{OH}$ obtained in step (b) into $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$ or $-\text{CH}_2-\text{O}-\text{PO}(\text{OH})_2$ or salts thereof in a manner known per se;
- (d) optionally conversion to a desired salt;
- (e) removing the protective group B.

In the above process, said protective group B may be any group that allows to regenerate an hydroxy group at the position it is attached to. Said protective group B is preferably stable under the conditions of step (a) to step (d). Said protective group B is removed in step (e) of said process in order to generate a hydroxy group. Protective groups for hydroxy groups are known to the skilled person. Group B may for example form an acetal group together with the

remaining moiety of the compound of formula (II), (III) or (IV). Acetals can be hydrolysed under acidic conditions. Most preferably, group B is a 2-tetrahydropyranyl group.

In the above process, said group D is a precursor group convertible reductively to a $-CH_2-OH$ group. Group D may be a derivative of a carbon acid. Examples of such a group include alkoxycarbonyl and aminocarbonyl groups. Said aminocarbonyl groups may be substituted at the amino group with one or two alkyl groups. It is most preferred to use alkoxycarbonyl groups. The alkyl group of said alkoxycarbonyl groups or said alkyl groups of said aminocarbonyl groups may be a linear or branched alkyl groups which may be singly or multiply substituted. Preferred are C_1-C_6 alkyl groups like methyl, ethyl, propyl, butyl, pentyl or hexyl groups. Most preferred are methyl or ethyl groups. The most preferred example of said group D is an ethoxycarbonyl group.

Said compound of formula (II) may be prepared by protecting the hydroxy group of hydroxy acetone with said group B. If group B is a tetrahydropyranyl group, the compound of formula (II) may be prepared from hydroxy acetone and 3,4-dihydro-2H-pyran, preferably employing pyridinium toluene-4-sulfonate as a catalyst. A specific method for preparing acetonyl tetrahydropyranyl ether is described in example 24.

In step (a) of said process, the compound of formula (II) is converted to a compound of formula (III) or (IV) by a Wittig or a Horner reagent. Wittig-type reactions and reagents are known to skilled persons (see e.g. Watanabe *et al.* 1996 and references cited therein). Common Wittig reagents to be used for the above process are methylenetriphenylphosphoranes which may be substituted at the methylene group. For the above process of this invention, a methylenetriphenylphosphorane is employed which is substituted with the above-defined group D at the methylene group. Such Wittig reagents are commercially available or can be prepared according to known methods.

The olefin produced in step (a) may be formed as a mixture of the cis/trans isomers of formulas (III) and (IV). If one of said isomers is preferred, it may be enriched or separated from the other isomer by methods known in the art, preferably by chromatography. Alternatively, a separation of said isomers may be carried out after one of the following steps (b) to (e).

In step (b) of the above process, group D of the compound of formula (III) or (IV) or a mixture of said compounds is reductively converted to a $-CH_2-OH$ group. Various methods are known

in the art to perform such a reduction. Conditions are chosen such that group D is reduced whereas the olefin moiety is not. Examples for reductants to be used in this step are molecular hydrogen or metal hydrides. Examples for useful metal hydrides include boron hydrides like sodium borohydride, aluminium hydrides like lithium aluminium hydride or diisobutyl aluminiumhydride (DIBAH), alkali metal or metal earth hydrides like sodium hydride or calcium hydride. Aluminium hydrides are preferred. A specific example for carrying out step (b) is described in example 24.

If the desired end product of said process is a compound of formula (I), wherein R^1 or R^2 is $-CH_2-OH$, the compound or mixture of compounds obtained in step (b) may be directly subjected to step (d) or step (e). Preferably, it is subjected to step (e) for removing protective group B. If the desired end product of said process is a compound of formula (I), wherein R^1 or R^2 is $-CH_2-O-PO(OH)-O-PO(OH)_2$ or $-CH_2-O-PO(OH)_2$, compound or mixture of compounds obtained in step (b) is subjected to step (c) of said process for converting $-CH_2-OH$ group obtained in step (b) into a $-CH_2-O-PO(OH)-O-PO(OH)_2$ or a $-CH_2-O-PO(OH)_2$ group.

Step (c) may be carried in several ways which are known to the skilled person. Step (c) may comprise substituting the hydroxy group of said $-CH_2-OH$ group obtained in step (b) by a leaving group. Step (c) may comprise converting said $-CH_2-OH$ group to a $-CH_2$ -halide group by a halogenating agent. A sulfuric, sulfonic or phosphoric acid halogenide may be employed as halogenating agent. Tosyl chloride is most preferred. Said halide may be fluoride, chloride, bromide or iodide, preferably chloride. The compound carrying said $-CH_2$ -halide group is preferably isolated. Said leaving group may further be created by reacting said $-CH_2-OH$ group obtained in step (b) with a sulfonic acid halide, preferably tosyl chloride.

Said intermediate having said leaving group may then be reacted with phosphoric or diphosphoric acid or singly or multiply deprotonated forms thereof. Preferably an alkylammonium salt of phosphoric or diphosphoric acid is used, more preferably a tetraalkylammonium salt, and most preferably a tetra-butylammonium salt. A polar aprotic solvent is preferred for this reaction. Preferably, the compound or mixture of compounds obtained is purified according to standard procedures. A specific example for carrying out step (c) is described in example 24.

In step (d), the compound or mixture of compounds obtained in step (c) may be converted to a desired salt. Methods for carrying out step (d) are well known. Such methods may comprise

adjusting the pH of an aqueous solution with an appropriate acid or salt to a desired pH value.

In step (e), the protective group B of a compound obtained in one of steps (b) to (d) is removed in order to obtain a compound of formula (I) wherein A is $-\text{CH}_2-\text{OH}$. The method for removing a protective group depends on the type of the protective group. Such methods are well known. If the protective groups forms an acetal, removing said protecting group may be achieved by acid hydrolysis (see example 24).

This invention provides protein in a form that is functional for the enzymatic conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate notably in its (*E*)-form, preferably in the presence of NADH and/or NADPH and/or in the presence of Co^{2+} . Said enzyme preferably has a sequence encoded by the *ispG* (formerly *gcpE*) gene of *E. coli* or a function-conservative homologue of said sequence, i.e. said homologue is capable of performing the same function as said protein. For many applications of said protein, it may be expressed and purified as a fusion protein, notably a fusion with maltose binding protein. In this way, enzymatically active protein may be readily obtained.

This invention further provides a protein in a form that is functional for the enzymatic conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its (*E*)-form, to isopentenyl diphosphate and/or dimethylallyl diphosphate. Said protein preferably requires FAD and NAD(P)H for said functionality. Further, said protein may require a metal ion selected from the group of manganese, iron, cobalt, or nickel ion. Said protein preferably has a sequence encoded by the *ispH* (formerly *lytB*) gene of *E. coli* or a function-conservative homologue of said sequence. For many applications of said protein, it may be expressed and purified as a fusion protein, notably a fusion with maltose binding protein. In this way, enzymatically active protein may be readily obtained.

The above proteins may be plant proteins, notably from *Arabidopsis thaliana*, bacterial proteins, notably from *E. coli*, or protozoal proteins, notably from *Plasmodium falciparum*.

The invention further provides a purified isolated nucleic acid encoding one or both of the above proteins with or without introns. Further, the invention provides a DNA expression vector containing the sequence of said purified isolated nucleic acid.

The invention further provides cells, cell cultures, organisms or parts thereof recombinantly endowed with the sequence of said purified isolated nucleic acid or with said DNA expression vector, wherein said cell is selected from the group consisting of bacterial, protozoal, fungal, plant, insect and mammalian cells. Said cells, cell cultures, organisms or parts thereof may further be endowed with at least one gene selected from the following group: *dxs*, *dxr*, *ispD* (formerly *ygbP*); *ispE* (formerly *ychB*); *ispF* (formerly *ygbB*) of *E. coli* or a function-conservative homologue thereof, or a function-conservative fusion, deletion or insertion variant of any of the above genes.

The invention further provides cells, cell cultures, or organisms or parts thereof transformed or transfected for an increased rate of formation of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its (E)-form, compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection. The transformation or transfection preferably comprises endowment with the *gcpE* gene of *E. coli* or with a function-conservative homologue from an other organism, e.g. plant or protozoal organism.

The invention also provides cells, cell cultures, or organisms or parts thereof transformed or transfected for an increased rate of conversion of (E)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate to isopentenyl diphosphate and/or dimethylallyl diphosphate compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection. The transformation or transfection preferably comprises endowment with the *lytB* gene of *E. coli* or with a function-conservative homologue from an other organism, e.g. plant or protozoal organism.

The invention provides also cells, cell cultures, or organisms or parts thereof transformed or transfected for an increased expression level of the protein of one of claims 1 to 4 and/or the protein of one of claims 5 to 8 compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection.

Moreover, the invention provides a method of altering the expression level of the gene product(s) of *ispG* and/or *ispH* or function-conservative homologues from other organisms or variants thereof in cells comprising

- (a) transforming host cells with the *ispG* and/or *ispH* gene,
- (b) growing the transformed host cells of step (a) under conditions that are suitable for the

efficient expression of *ispG* and/or *ispH*, resulting in production of altered levels of the *ispG* and/or *ispH* gene product(s) in the transformed cells relative to expression levels of untransformed cells.

Furthermore, the invention provides a method of identifying an inhibitor of an enzyme functional for the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably its *E*-form, of the non-mevalonate isoprenoid pathway by the following steps:

- (a) incubating a mixture containing said enzyme with its, optionally isotope-labeled, substrate 2C-methyl-D-erythritol-2,4-cyclodiphosphate under conditions suitable for said conversion in the presence and in the absence of a potential inhibitor,
- (b) subsequently determining the concentration of 2C-methyl-D-erythritol 2,4-cyclodiphosphate and/or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, and
- (c) comparing the concentration in the presence and in the absence of said potential inhibitor.

Furthermore, the invention provides a method of identifying an inhibitor of an enzyme functional for the conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably its *E*-form, to isopentenyl diphosphate or dimethylallyl diphosphate of the non-mevalonate isoprenoid pathway by the following steps:

- (a) incubating a mixture containing said enzyme with its, optionally isotope-labeled, substrate 1-hydroxy-2-methyl-2-butenyl 4-diphosphate under conditions suitable for said conversion in the presence and in the absence of a potential inhibitor, whereby said mixture preferably contains FAD,
- (b) determining the concentration of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate or dimethylallyl diphosphate, and
- (c) comparing the concentration in the presence and in the absence of said potential inhibitor.

The above methods of identifying an inhibitor are preferably carried out by following the consumption of NADPH or NADH making use of its characteristic absorbance spectrum. Alternatively, the fluorescence of NADH or NADPH can be followed when excited around 340 nm. The above methods of identifying an inhibitor may advantageously be performed as high-

throughput screening assays for inhibitors, notably in combination with photometric detection of the consumption of NADH or NADPH. Further, one or more flavin analogues (e.g. FAD, FMN) may be added to the incubation mixtures in said methods, preferably in catalytic amounts. Most preferred is the addition of FAD. Said enzymes may be employed in said methods as fusion proteins with maltose binding protein (examples 38 to 41, 44, 45), which allows straightforward expression and purification of said enzymes in enzymatically active form. Further embodiments of said methods of identifying are defined in the subclaims to these methods.

It is known that intermediates of the non-mevalonate pathway are responsible for $\gamma\delta$ T cell activation by various pathogenic bacteria. $\gamma\delta$ T cell activation is followed by T cell proliferation, secretion of cytokines and chemokines and is very likely crucial for regulating the immune response following pathogen infection (Altincicek *et al.*, 2001 and references cited therein). Recently, it was shown that *E. coli* strains lost the ability to stimulate $\gamma\delta$ T cells when the *dxr* or the *gcpE* gene was knocked out, strongly indicating that an intermediate downstream of *gcpE* and upstream of isopentenyl pyrophosphate exhibits the most potent antigenic activity (Altincicek *et al.*, 2001). However, the intermediate produced by the *gcpE* gene product in the pathway has been unknown. Herein, this intermediate has surprisingly been identified as an hitherto unprecedented compound, which opens up a whole range of novel applications for this compound.

The compounds of formula I can be used as immunomodulatory or immunostimulating agents, e.g. for activating $\gamma\delta$ T cells. Immunomodulation via $\gamma\delta$ T cell activation by said compounds may prove useful not only to support combat against pathogens but for various conditions for which a stimulation of the immune system is desirable. The novel compounds of the invention may therefore be used for medical treatment of pathogen infections. Such a treatment stimulates the activity of the immune system against the pathogen. Preferably, the compound wherein $R^1=H$ and/or A is $-CH_2OH$ is used for this application. Alternatively, the oxidation product with A = CHO may prove to be highly active. Among the compounds of formula I, the one with the highest or most suitable $\gamma\delta$ T cell stimulating activity may be selected in a test system known in the art (e.g. that described by Altincicek *et al.*, 2001). Importantly, since the compounds of the invention do not act as antibiotics, development of resistancies is not a problem for the method of treatment disclosed herein.

In an advantageous embodiment, said compounds may be combined with an antibiotically active compound for treating a pathogen infection. Such a treatment combines the advantages of inhibiting pathogen proliferation by an antibiotic and stimulating the immune system against the pathogen resulting in a much faster and more efficient treatment. Such an antibiotically active compound may be a bacteriostatic antibiotic (e.g. tetracyclines).

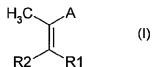
Therefore, the novel compounds of this invention may be used for the preparation of a medicament. The invention further pertains to a pharmaceutical composition containing a compound of formula I and a pharmaceutically acceptable carrier. Said pharmaceutical composition may further contain an antibiotically active compound as mentioned above.

This invention further comprises antibodies against the compounds of formula I. Said antibodies may be polyclonal or monoclonal and may be raised according to conventional techniques. Raising such antibodies will comprise coupling of a compound of formula I has hapten to a macromolecular carrier like a protein in order to be immunogenic. Such an immunogenic compound of formula I may further be used as a vaccine.

The antibodies of the invention may be used for detecting a compound of formula I. Since said compounds are produced by organisms having the non-mevalonate isoprenoid pathway, such organisms may be detected using said antibodies. Preferably, such organisms may be detected in body fluids in a diagnostic method, thereby indicating an infection by a pathogen having the non-mevalonate pathway. A positive result in such a diagnostic method may at the same time indicate possible treatment by the compounds of the invention.

When an antibody of the invention is used for detecting a compound of formula I, it is preferably labelled to allow photometric detection and/or immobilized to a support. Such methods are well-known in the art.

This invention further provides a process for the chemical preparation of a compound of formula I or a salt thereof (see Fig. 7):



wherein A represents $-\text{CH}_2\text{OH}$ or $-\text{CHO}$, R^1 is hydrogen, and R^2 is $-\text{CH}_2\text{O}-\text{PO}(\text{OH})-\text{O}-$

$\text{PO}(\text{OH})_2$, $-\text{CH}_2\text{-O-PO}(\text{OH})_2$ or $-\text{CH}_2\text{-OH}$ by the following steps:

- (a) converting 2-methyl-2-vinyl-oxiran into 4-chloro-2-methyl-2-buten-1-al;
- (b) converting 4-chloro-2-methyl-2-buten-1-al to its acetal;
- (c) substituting the chlorine atom in the product of step (b) by a hydroxyl group, a phosphate group or a pyrophosphate group;
- (d) hydrolysing the acetal obtained in step (c) to produce an aldehyde group;
- (e) optionally converting the aldehyde group of the product of step (d) to a $-\text{CH}_2\text{OH}$ group.

Preferred embodiments of this process are defined in the subclaims and are exemplified in example 42.

The invention will now be described in detail with reference to specific examples.

Example 1

Construction of a vector carrying the *xylB* gene of *Escherichia coli* capable for transcription and expression of D-xylulokinase

Chromosomal DNA from *Escherichia coli* strain XL1-Blue (Bullock et al. 1987; commercial source: Stratagene, LaJolla, CA, USA) is isolated according to a method described by Meade et al. 1982.

The *E. coli* ORF *xylB* (accession no. gb AE000433) from base pair (bp) position 8596 to 10144 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CCGTCGGAATTCGAGGAGAAATTAACCATGTATATCGGGATAGATCTTGG-3', 10 pmol of the primer 5'-GCAGTGAAGCTTTTACGCCATTAATGGCAGAAGTTGC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec, Seraing, Belgium) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 75 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplicate is purified with the PCR purification kit from Qiagen (Hilden, Germany).

1.0 µg of the vector pBluescript SKI⁺ (Stratagene) and 0.5 µg of the purified PCR product are digested with *Eco*RI and *Hind*III in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (New England Biolabs, Frankfurt am Main, Germany (NEB)) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 20 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBSxylB. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells according to a method described by Dower et al., 1988. The plasmid pBSxylB is isolated with the plasmid

isolation kit from Qiagen.

The DNA insert of the plasmid pBSxylB is sequenced by the automated dideoxynucleotide method (Sanger *et al.*, 1992) using an ABI Prism 377™ DNA sequencer from Perkin Elmer (Norwalk, USA) with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions (Foster city, USA). It is identical with the DNA sequence of the database entry (gb AE000433).

Example 2

Construction of a vector carrying the *xylB* and *dxr* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase and DXP reductoisomerase

The *E. coli* ORF *dxr* (accession no. gb AE000126) from base pair (bp) position 9887 to 11083 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CTAGCCAAGCTTGAGGAGAAATTAACCATGAAGCAACTCACCATTCTGG-3', 10 pmol of the primer 5'-GGAGATGTGCGACTCAGCTTGCGAGACGC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 75 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

1.2 µg of the vector pBSxylB (Example 1) and 0.6 µg of the purified PCR product are digested with *Hind*III and *Sal*I in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 18 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 μ l of T4-Ligase buffer (Gibco) in a total volume of 10 μ l, yielding the plasmid pBSxylBdxr. The ligation mixture is incubated for 2 h at 25 °C. 1 μ l of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBSxylBdxr is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBSxylBdxr is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000126).

The DNA sequence of the vector construct pBSxylBdxr is shown in Annex A.

Example 3

Construction of a vector carrying the *xylB*, *dxr* and *ispD* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXP reductoisomerase and CDP-ME synthase

The *E. coli* ORF *ispD* (accession no. gb AE000358) from base pair (bp) position 6754 to 7464 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CCGGGAGTCGACGAGGAGAAATTAACCATGGCAACCACTCATTTGGATG-3', 10 pmol of the primer 5'-GTCCAACCTCGAGTTATGTATTCTCCTTGATGG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 μ l containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 30 sec at 94 °C, 30 sec at 50 °C and 45 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 μ l is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

1.5 μ g of the vector pBSxylBdxr (Example 2) and 0.8 μ g of the purified PCR product are digested with *Sal*I and *Xho*I in order to produce DNA fragments with overlapping ends. The

restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 12 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBSxylBdxrispD. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBSxylBdxrispD is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBSxylBdxrispD is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000126).

The DNA sequence of the vector construct pBSxylBdxrispD is shown in Annex B.

Example 4

Construction of a vector carrying the *xylB*, *dxr*, *ispD* and *ispF* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXP reductoisomerase, CDP-ME synthase, and cMEPP synthase

The *E. coli* ORF's *ispD* and *ispF* (accession no. gb AE000358) from base pair (bp) position 6275 to 7464 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CCGGGAGTCGACGAGGAGAAATTAACCATGGCAACCACTCATTTGGATG-3', 10 pmol of the primer 5'-TATCAACTCGAGTCATTTTGTTCCTTAATGAG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 75 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

1.4 µg of the vector pBSxylBdxr (Example 2) and 0.7 µg of the purified PCR product are digested with *Sall* and *XhoI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 18 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBSxylBdxrispDF. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBSxylBdxrispDF is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBSxylBdxrispDF is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000126).

Example 5

Construction of a vector carrying the *xylB*, *dxr*, *ispD*, *ispE* and *ispF* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXP reductoisomerase, CDP-ME synthase, CDP-ME kinase and cMEPP synthase

The *E. coli* ORF *ispE* (accession no. gb AE000219) from base pair (bp) position 5720 to 6571 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5' - GCGAACCCTCGAGGAGGAGAAATTAACCATGCGGACACAGTGGCCC-3', 10 pmol of the primer 5'-CCTGACGGTACCTTAAAGCATGGCTCTGTGC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

1.2 µg of the vector pBSxylBdxrispDF (Example 4) and 0.6 µg of the purified PCR product are digested with *XhoI* and *KpnI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 15 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBS_{cyclo}. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBS_{cyclo} is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBS_{cyclo} is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000219). The DNA sequence of the vector construct pBS_{cyclo} is shown in Annex C.

Example 6

Construction of a vector carrying the *gcpE* gene of *Escherichia coli* capable for its transcription and expression

The *E. coli* ORF *gcpE* (accession no. gb AE000338) from base pair (bp) position 372 to 1204 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CGTACCGGATCCGAGGAGAAATTAACCATGCATAACCAGGCTCCAATTC-3', 10 pmol of the primer 5'-CCCATCGTCGACTTATTTTCAACCTGCTGAACGTC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of

100 μ l containing 1.5 mM $MgCl_2$, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 μ l is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.0 μ g of the vector pACYC184 (Chang and Cohen 1978, NEB) and 0.7 μ g of the purified PCR product are digested with *Bam*HI and *Sal*I in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 20 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 μ l of T4-Ligase buffer (Gibco) in a total volume of 10 μ l, yielding the plasmid pACYCgcpE. The ligation mixture is incubated for 2 h at 25 °C. 1 μ l of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYCgcpE is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYCgcpE is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000338).

The DNA sequence of the vector construct pACYCgcpE is shown in Annex D.

Example 7

Construction of vectors carrying a carotenoid operon from *Erwinia uredovora* capable for the *in vivo* production of β -carotene

The open reading frames *crtY*, *crtI* and *crtB* of a carotenoid operon from *Erwinia uredovora* (accession no. gb D90087) from base pair (bp) position 2372 to 6005 is amplified by PCR

using chromosomal *E. uredoovora* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CATTGAGAAGCTTATGTGCACCG-3', 10 pmol of the primer 5'-CTCCGGGGTCGACATGGCGC-3', 40 ng of chromosomal DNA of *E. uredoovora*, 8 U of Taq DNA polymerase (Eurogentec), 20 nmol of dNTPs, Taq Extender (Stratagene) in a total volume of 100 µl 1x Taq Extender buffer (Stratagene).

The mixture is denaturated for 3 min at 94 °C. Then 40 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 300 sec at 72 °C followed. After further incubation for 20 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden, Germany).

1.0 µg of the vector pBluescript SKII⁺ (Stratagene) and 2.0 µg of the purified PCR product are digested with *Hind*III and *Sall* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 40 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBScaro34. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBScaro34 is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBScaro34 is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb D90087).

The *E. uredoovora* ORF *crfE* (accession no. gb D90087) from base pair (bp) position 175 to 1148 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CCGCATCTTTCCAATTGCCG-3', 10 pmol of the primer 5'-ATGCAGCAAGCTTAAGTACGCGC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA

polymerase (Eurogentec, Seraing, Belgium) and 20 nmol of dNTPs in a total volume of 100 μ l containing 1.5 mM $MgCl_2$, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 μ l is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden, Germany).

1.5 μ g of the vector pBScaro34 (see above) is digested with *EcoRI* and *HindIII* and 0.6 μ g of the purified PCR product are digested with *MfeI* and *HindIII* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 16 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 μ l of T4-Ligase buffer (Gibco) in a total volume of 10 μ l, yielding the plasmid pBScaro14. The ligation mixture is incubated for 2 h at 25 °C. 1 μ l of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBScaro14 is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBScaro14 is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb D90087). The DNA sequence of the plasmid pBScaro14 is shown in Annex E.

5 μ g of the vector pBScaro14 (see above) is digested with *BamHI* and *Sall*. The restriction mixture is prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. The restriction mixture is separated on a agarose gel and the fragments of 2237 and 2341 bp size are purified with the gel extraction kit from Qiagen.

3 μ g of the vector pACYC184 (see above) is digested with *BamHI* and *Sall*. The restriction

mixture is prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. The restriction mixture is separated on a agarose gel and the fragment of 3968 bp size is purified with the gel extraction kit from Qiagen.

30 ng of the purified vector DNA and each 25 ng of the purified 2237 and 2341 bp fragments are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYCcaro14. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYCcaro14 is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYCcaro14 is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb D90087). The DNA sequence of the plasmid pACYCcaro14 is shown in Annex F.

Example 8

Enzymatic preparation of [U-¹³C₆]1-deoxy-D-xylulose 5-phosphate

A reaction mixture containing 960 mg of [U-¹³C₆]glucose (5.1 mmol), 6.1 g of ATP (10.2 mmol), 337 mg of thiamine pyrophosphate, 1.14 g of [2,3-¹³C₂]pyruvate (10.2 mmol), 10 mM MgCl₂, 5 mM dithiothreitol in 150 mM Tris hydrochloride, pH 8.0 is prepared. 410 Units of triose phosphate isomerase (from rabbit muscle, Type III-S, E. C. 5.3.1.1., Sigma), 100 U hexokinase (from Bakers Yeast, Type VI, E. C. 2.7.1.1, Sigma), 100 U phosphoglucose isomerase (from Bakers Yeast, Type III, E. C. 5.3.1.9, Sigma), 100 U phosphofructokinase (from *Bacillus stearothermophilus*, Type VII, E. C. 2.7.1.11, Sigma), 50 U aldolase (from rabbit muscle, E. C. 4.1.2.13, Sigma) and 12 U of recombinant DXP synthase from *B. subtilis* are added to a final volume of 315 ml. The reaction mixture is incubated at 37 °C overnight and during incubation the pH is held at a constant value of 8.0. The reaction is monitored by ¹³C NMR spectroscopy.

Example 9

Enzymatic preparation of [3,4,5-¹³C₃]1-deoxy-D-xylulose 5-phosphate

A solution containing 150 mM Tris hydrochloride, 10 mM MgCl₂, 1.0 g of [U-¹³C₆]glucose (5.4 mmol), 0.23 g (1.5 mmol) of dithiothreitol, 0.3 g (0.7 mmol) of thiamine pyrophosphate, 0.1 g (0.2 mmol) of ATP (disodium salt), and 2.2 g (11mmol) of phosphoenol pyruvate (potassium salt) is adjusted to pH 8.0 by the addition of 8 M sodium hydroxide. 403 U (2.8 mg) of pyruvate kinase (from rabbit muscle, E. C. 2.7.1.40), 410 Units of triose phosphate isomerase (from rabbit muscle, Type III-S, E. C. 5.3.1.1., Sigma), 100 U hexokinase (from Bakers Yeast, Type VI, E. C. 2.7.1.1, Sigma), 100 U phosphoglucose isomerase (from Bakers Yeast, Type III, E. C. 5.3.1.9, Sigma), 100 U phosphofructokinase (from *Bacillus stearothermophilus*, Type VII, E. C. 2.7.1.11, Sigma), 50 U aldolase (from rabbit muscle, E. C. 4.1.2.13, Sigma) and 12 U recombinant DXP synthase from *B. subtilis* are added to a final volume of 300 ml. The reaction mixture is incubated at 37 °C for overnight.

Example 10

Enzymatic preparation of 1-deoxy-D-xylulose

The pH value of the reaction mixture obtained in example 8 or 9 is adjusted to 9.5. Magnesium chloride is added to a concentration of 30 mM. 50 mg (950 Units) of alkaline phosphatase from bovine intestinal mucosa (Sigma, E. C. 3.1.3.1) are added and the reaction mixture is incubated for 16 h. The conversion is monitored by ¹³C-NMR spectroscopy. The pH is adjusted to a value of 7.0 and the solution is centrifuged at 14,000 upm for 5 minutes. Starting from labelled glucose (examples 8 or 9) the overall yield of 1-deoxy-D-xylulose is approximately 50 %.

The supernatant or the lyophilised supernatant is used in incorporation experiments (see examples 11 to 17).

Example 11

Incorporation experiment with recombinant *Escherichia coli* XL1-pBSxylB using [3,4,5-¹³C₃]1-deoxy-D-xylulose

0.2 litre of Luria Bertani (LB) medium containing 36 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harbouring the plasmid pBSxylB (see example 1). The cells are grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.6 the culture is induced with 2 mM IPTG. Two hours after induction with IPTG, 50 ml (0.9 mmol) of

crude [3,4,5-¹³C₃]1-deoxy-D-xylulose (pH 7.0) (see examples 9 and 10), are added. Aliquots of 25 ml are taken at time intervals of 30 minutes and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 µl of 20 mM NaF in D₂O, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. ¹³C NMR spectra of the supernatant are recorded directly, without further purification, with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). The NMR analysis is based on published signal assignments (Wungsintaweekul *et al.*, 2001).

30 min after the addition of [3,4,5-¹³C₃]1-deoxy-D-xylulose, the formation of [3,4,5-¹³C₃]1-deoxy-D-xylulose 5-phosphate can be observed. The maximum yield of [3,4,5-¹³C₃]1-deoxy-D-xylulose 5-phosphate is observed 3-5 h after addition of [3,4,5-¹³C₃]1-deoxy-D-xylulose to the medium. The ¹³C NMR signals reveal a mixture of [3,4,5-¹³C₃]1-deoxy-D-xylulose and [3,4,5-¹³C₃]1-deoxy-D-xylulose-5-phosphate at a molar ratio of approximately 1 : 9. The intracellular concentration of [3,4,5-¹³C₃]1-deoxy-D-xylulose 5-phosphate is estimated as 20 mM by quantitative NMR spectroscopy.

Example 12

Incorporation experiment with recombinant *Escherichia coli* XL1-pBSxyIBdxr using [U-¹³C₃]1-deoxy-D-xylulose

0.12 litre of Luria Bertani (LB) medium containing 22 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harbouring plasmid pBSxyIBdxr (see example 2). The cells are grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.6 the culture is induced with 2 mM IPTG. Two hours after induction with IPTG, ca. 1.0 mmol of crude [U-¹³C₃]1-deoxy-D-xylulose (pH 7.0) (see examples 8 and 10) are added. Aliquots of 25 ml are taken in time intervals of 1 h and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 µl of 20 mM NaF in D₂O, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the supernatant are recorded directly, without further purification, with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany).

HMQC and HMQC-TOCSY experiments reveal ^1H - ^{13}C and ^1H - ^1H spin systems (Table 1) of [$\text{U-}^{13}\text{C}_5$]2C-methyl-D-erythritol 4-phosphate, [$\text{U-}^{13}\text{C}_5$]2C-methyl-D-erythritol and [1,2,2',3,4- $^{13}\text{C}_5$]4-diphosphocytidyl-2C-methyl-D-erythritol at a molar ratio of approximately 6.6 : 7 : 1, respectively. The intracellular concentration of [$\text{U-}^{13}\text{C}_5$]2C-methyl-D-erythritol 4-phosphate is estimated as 10 mM by quantitative NMR spectroscopy.

The NMR data summarized in Table 1 are identical with published NMR data of the authentic compounds (Takahashi et al., 1998; Rohdich et al., 1999).

Table 1. NMR data of ^{13}C -labeled products in cell extracts of *E. coli* XL1-pBSxyIbDxr after feeding of [$\text{U-}^{13}\text{C}_5$]1-deoxy-D-xylulose

Chemical shifts, ppm						
Position	1	1*	2	2-Methyl	3	4
[$\text{U-}^{13}\text{C}_5$]2C-methyl-D-erythritol 4-phosphate						
^{13}C	66.1	n.d.	18.1	73.4		648
^1H	3.25	3.36	0.93	3.56	3.62	3.81
[$\text{U-}^{13}\text{C}_5$]2C-methyl-D-erythritol						
^{13}C	66.6	n.d.	18.0	74.6		616
^1H	3.26	3.34	0.9	3.44	3.36	3.61
[1,2,2',3,4- $^{13}\text{C}_5$]4-diphosphocytidyl-2C-methyl-D-erythritol						
^{13}C	66.8	n.d.	18.0	73.0		667
^1H	3.4	3.55	0.9	3.6	3.74	4

Example 13

Incorporation experiment with recombinant *Escherichia coli* XL1-pBSxyIbDxrspDF using [3,4,5- $^{13}\text{C}_3$]1-deoxy-D-xylulose

0.1 litre of Luria Bertani (LB) medium containing 18 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harbouring the plasmid pBSxyIbDxrspDF (see example 4). The cells are grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.5, the culture is induced with 2 mM IPTG. Two hours after induction with IPTG, ca. 1.0 mmol of crude [3,4,5- $^{13}\text{C}_3$]1-deoxy-D-xylulose (see examples 9 and 10) are added. After three

hours, cells were harvested and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 1.5 ml of 20 mM NaF in D₂O, cooled on ice and sonified 3 x 15 sec. with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the supernatant are recorded directly, without further purification, with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany).

HMQC and HMQC-TOCSY experiments reveal ¹H-¹³C and ¹H-¹H spin systems of [1,3,4-¹³C₃]2C-methyl-D-erythritol 4-phosphate, [1,3,4-¹³C₃]2C-methyl-D-erythritol and [1,3,4-¹³C₃]4-diphosphocytidyl-2C-methyl-D-erythritol (Table 1). The molar ratios of [1,3,4-¹³C₃]2C-methyl-D-erythritol 4-phosphate, [1,3,4-¹³C₃]2C-methyl-D-erythritol and [1,3,4-¹³C₃]4-diphosphocytidyl-2C-methyl-D-erythritol are 1 : 0.6 : 0.9, respectively.

This result indicates that the intracellular amount of CTP required for the synthesis of 4-diphosphocytidyl-2C-methyl-D-erythritol is limiting. Therefore, a modified fermentation protocol was developed (see example 14).

Example 14

Incorporation experiment with recombinant *Escherichia coli* XL1-pBSxylBdxrpsDF using [3,4,5-¹³C₃]1-deoxy-D-xylulose

0.1 litre of Luria Bertani (LB) medium containing 18 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harbouring plasmid pBSxylBisDF (see example 4). The cells are grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.5, the culture is induced with 2 mM IPTG. Two hours after induction with IPTG, 10 mg (0.041 mmol) of cytidine and 5 ml of 1 M NaH₂PO₄, pH 7.2, and ca. 1 mmol of crude [3,4,5-¹³C₃]1-deoxy-D-xylulose (see examples 9 and 10) are added. After three hours, the cells are harvested and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 µl of 20 mM NaF in D₂O, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the supernatant are recorded directly, without further purification, with a Bruker AVANCE DRX 500 spectrometer. HMQC and HMQC-TOCSY experiments reveal ¹H-¹³C and ¹H-¹H spin systems (Table 1) of

[1,3,4- $^{13}\text{C}_3$]2C-methyl-D-erythritol 4-phosphate, [1,3,4- $^{13}\text{C}_3$]2C-methyl-D-erythritol and [1,3,4- $^{13}\text{C}_3$]4-diphosphocytidyl-2C-methyl-D-erythritol at a molar ratio of approximately 1 : 3.4 : 4.2, respectively. The relative amount of [1,3,4- $^{13}\text{C}_3$]4-diphosphocytidyl-2C-methyl-D-erythritol is increased by a factor of 2 as compared to the relative amount in example 13. The intracellular concentration of [1,3,4- $^{13}\text{C}_3$]4-diphosphocytidyl-2C-methyl-D-erythritol is estimated as 10 mM by quantitative NMR spectroscopy. The relative high amount of 2C-methyl-D-erythritol indicates that unspecific phosphatases convert intermediary formed 2C-methyl-D-erythritol 4-phosphate into 2C-methyl-D-erythritol. Therefore, a modified fermentation protocol was developed to supply the cells with sufficient amounts of organic phosphates and in order to suppress the activity of phosphatases (see examples 15 to 17).

Example 15

Incorporation experiment with recombinant *Escherichia coli* XL1-pBS_{cyclo} using [U- $^{13}\text{C}_6$]1-deoxy-D-xylulose

0.2 litre of Luria Bertani (LB) medium containing 36 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harbouring the plasmid pBS_{cyclo} (see example 5). The cells are grown in a shaking culture at 37 °C. At an optical density (600 nm) of 1.3, the culture is induced with 2 mM IPTG. Two hours after induction with IPTG, 30 mg (0.12 mmol) of cytidine, 300 mg (0.95 mmol) of DL- α -glycerol 3-phosphate and 10 ml of 1 M NaKHPO_4 , pH 7.2, are added. After 30 min, ca. 1 mmol of [U- $^{13}\text{C}_6$]1-deoxy-D-xylulose (see example 8 and 10) are added. Aliquots of 25 ml are taken at time intervals of 1 h and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 μl of 20 mM NaF in D_2O , cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the cell free extract are recorded directly, without further purification, with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). ^{13}C NMR spectra, as well as HMQC and HMQC-TOCSY spectra established [U- $^{13}\text{C}_6$]2C-methyl-D-erythritol 2,4-cyclodiphosphate (Herz *et al.*, 2000) as the only product. Formation of [U- $^{13}\text{C}_6$]2C-methyl-D-erythritol 2,4-cyclodiphosphate can be observed 30 min after addition of [U- $^{13}\text{C}_6$]1-deoxy-D-xylulose, whereas the maximum yield is observed 5 h after addition of [U- $^{13}\text{C}_6$]1-deoxy-D-xylulose. The intracellular concentration of [U- $^{13}\text{C}_6$]2C-methyl-D-

erythritol 2,4-cyclodiphosphate is estimated as 20 mM by quantitative NMR spectroscopy. The formation of any other isotope-labelled products, such as $[U-^{13}C_3]2C$ -methyl-erythritol is completely suppressed.

Example 16

Incorporation experiment with recombinant *Escherichia coli* XL1-pBS_{cyclo}-pACYCgcpE using $[2-^{14}C]$ - and $[U-^{13}C_3]1$ -deoxy-D-xylulose

0.2 litre of Terrific Broth (TB) medium containing 36 mg of ampicillin and 2.5 mg of chloramphenicol are inoculated with the *E. coli* strain XL1-Blue harbouring the plasmids pBS_{cyclo} and pACYCgcpE (see example 5 to 6). The cells are grown in a shaking culture at 37 °C overnight. At an optical density (600 nm) of 4.8 to 5.0, 30 mg (0.1 mmol) of cytidine, 300 mg (0.94 mmol) of DL- α -glycerol 3-phosphate and 10 ml of 1 M NaH₂PO₄, pH 7.2, are added. After 30 minutes, a mixture of 2.6 μ mol $[2-^{14}C]1$ -deoxy-D-xylulose (15 μ Ci μ mol⁻¹) (Wungsintaweekul et al., 2001) and 1 ml of crude $[U-^{13}C_3]1$ -deoxy-D-xylulose (0.02 mmol) (see examples 8 and 10) are added. After 1.5 h, cells are harvested and centrifuged for 10 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in a mixture of 20 mM NaF (2 ml) and methanol (2 ml), cooled on ice and sonified 3 x 15 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4. The suspension is centrifuged at 15,000 rpm for 15 min. The radioactivity of the supernatant is measured by scintillation counting (Beckmann, LS 7800). 10 % of the radioactivity initially added as ^{14}C labelled 1-deoxy-D-xylulose is detected in the supernatant. Aliquots are analysed by TLC and HPLC, as described in example 19, and the products are purified as described in example 20. On basis of these data, 1-hydroxy-2-methyl-2-butenyl 4-diphosphate and 2-C-methyl-D-erythritol 2,4-cyclodiphosphate were identified as products at a molar ratio of 7 : 3 (see also examples 17 and 18).

Example 17

Incorporation experiment with recombinant *Escherichia coli* XL1-pBS_{cyclo}-pACYCgcpE using $[U-^{13}C_3]$ - or $[3,4,5-^{13}C_3]1$ -deoxy-D-xylulose

0.2 litre of Terrific Broth (TB) medium containing 36 mg of ampicillin and 2.5 mg of

chloramphenicol are inoculated with the *E. coli* strain XL1-Blue harbouring the plasmids pBScyco and pACYCgcpE. The cells are grown in a shaking culture at 37 °C for overnight. At an optical density (600 nm) of 4.8 - 5.0, 30 mg (0.1 mmol) of cytidine, 300 mg (0.93 mmol) of DL- α -glycerol 3-phosphate and 10 ml of 1 M NaKHPO₄, pH 7.2, are added. After 30 minutes, 3 ml of crude [3,4,5-¹³C]₃- or [U-¹³C₅]1-deoxy-D-xylulose (0.05 mmol) (see examples 8, 9, and 10) are added. Aliquots of 25 ml are taken at time intervals of 1 h and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 μ l of 20 mM NaF in D₂O or in 700 μ l of a mixture of methanol and D₂O (6:4; v/v) containing 10 mM NaF, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the cell free extracts are recorded directly with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). In order to avoid degradation during work-up, the structures of the products are determined by NMR spectroscopy without further purification (see example 18).

Example 18

Structure determination of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate

The ¹H-decoupled ¹³C NMR spectrum using [U-¹³C₅]1-deoxy-D-xylulose as starting material displays 5 ¹³C-¹³C coupled signals belonging to 2C-methyl-D-erythritol 2,4-cyclodiphosphate (Herz et al., 2000) and 5 ¹³C-¹³C coupled signals at 14.7, 64.5, 68.6, 122.7 and 139.5 ppm (Table 2) belonging to an unknown metabolite. The chemical shifts of the unknown metabolite suggest a double bond motif (signals at 122.7 and 139.5 ppm), a methyl group (signal at 14.7 ppm), and two carbon atoms (signals at 64.5 and 68.6 ppm) connected to OR (R=unknown). The three signals accounting for carbon atoms with sp³ hybridisation (14.7, 64.5 and 68.6 ppm) show ¹³C-¹³C coupling to one adjacent ¹³C atom with coupling constants of 40 - 50 Hz (Table 2). The signal at 122.7 ppm shows ¹³C couplings to two adjacent ¹³C neighbours (coupling constants, 74 and 50 Hz), whereas the signal at 141.5 ppm shows ¹³C couplings to three neighboured ¹³C atoms (coupling constants, 74, 43 and 43 Hz). In conjunction with the chemical shift topology, this coupling signature is indicative for a 2-methyl-2-butenyl skeleton. HMQC and HMQC-TOCSY experiments reveal the ¹H NMR chemical shifts (Table 2), as well as ¹³C-¹H and ¹H-¹H spin systems (Table 3). More specifically, the ¹³C NMR signal at 122.7

ppm correlates to a ^1H NMR signal at 5.6 ppm which is in the typical chemical shift range for H-atoms attached to CC double bonds, whereas the signal at 139.5 ppm gives no ^{13}C - ^1H correlations. The signals at 64.5 and 68.6 ppm give ^{13}C - ^1H correlations to ^1H -signals at 4.5 and 3.9 ppm, respectively. The methyl signal at 14.7 ppm correlates to a proton signal at 1.5 ppm. In connection with ^{13}C - ^{13}C coupling patterns (Table 2), as well as with ^1H - ^{13}C long range correlations (HMBC experiment, Table 3), these data establish a 1,4-dihydroxy-2-methyl-2-butenyl system.

Starting from [3,4,5- $^{13}\text{C}_3$]1-deoxy-D-xylulose as feeding material three signals at 64.5, 68.6 and 122.7 ppm accounting for atoms 4, 1 and 3, respectively, of the new product are observed. It can be concluded that the carbon atoms at 1, 3 and 4 of the new product are biogenetically equivalent to the carbon atoms 3, 4 and 5 of [3,4,5- $^{13}\text{C}_3$]1-deoxy-D-xylulose 5-phosphate. This coupling topology is similar to the coupling pattern of 2C-methyl-D-erythritol 4-phosphate (see example 13) confirming that the new compound is derived via 2C-methyl-D-erythritol 4-phosphate.

The C-4 and C-3 ^{13}C NMR signals at 64.5 and 122.7 ppm show ^{13}C - ^{31}P coupling of 5.5 and 8.0 Hz, respectively. These couplings indicate the presence of a phosphate or pyrophosphate group at position 4 of the 2-methyl-2-butenyl skeleton.

In line with this observation, the ^1H -decoupled ^{31}P NMR spectrum of the product displays a doublet at -9.2 (^3P - ^{31}P coupling constant, 20.9 Hz) and a double-double-doublet at -10.6 ppm (^3P - ^{13}C coupling constants, 5.8 and 7.4 Hz, ^{31}P - ^{31}P coupling constant, 20.9 Hz). Without ^1H -decoupling, the ^{31}P NMR signal at -10.6 ppm is broadened whereas the signal at -9.2 ppm is not affected by ^1H coupling. The chemical shifts as well as the observed coupling pattern confirm the presence of a free diphosphate moiety at position 4.

In summary, all these data establish the structure as 1-hydroxy-2-methyl-2-butenyl 4-diphosphate.

Table 2. NMR data of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate

Position	Chemical shifts, ppm			Coupling constants, Hz		
	$^1\text{H}^a$	$^{13}\text{C}^b$	$^{31}\text{P}^c$	J_{PC}	J_{PP}	J_{CC}
1	3.91	68.6 ^{d,e}				43.0 ^e , 5.5 ^d , 3.5 ^d
2		139.5 ^{d,e}				74.3 ^e , 43.3 ^e , 43.3 ^e
2-Methyl	1.51	14.7 ^e				42.2 ^e , 4.0 ^e , 4.0 ^e
3	5.57	122.7 ^e		8.0 ^d		73.9 ^e , 49.8 ^d , 4.0 ^d
4	4.46	64.5 ^{d,e}		5.5 ^d		49.3 ^e , 5.5 ^d
P_β			-9.2		20.9	
P_α			-10.6	5.8 ^d , 7.4 ^d	20.9	

^areferenced to external trimethylsilylpropane sulfonate.^breferenced to external trimethylsilylpropane sulfonate.^creferenced to external 85 % orthophosphoric acid.^dobserved with $[1,3,4\text{-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphate^eobserved with $[\text{U-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphateTable 3. Correlation pattern of $[1,3,4\text{-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphate and of $[\text{U-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphate

NMR Correlation pattern			
Position	HMQC	HMQC-TOCSY	HMBC
1	1 ^{a,b}	1 ^{a,b}	2-methyl ^a , 2 ^a
2			
2-methyl	2-methyl ^b	2-methyl ^a	
3	3 ^{a,b}	3 ^{a,b} , 4 ^{a,b}	2-methyl ^a , 1 ^a
4	4 ^{a,b}	4 ^{a,b} , 3 ^{a,b}	

^aobserved with $[1,3,4\text{-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphate^bobserved with $[\text{U-}^{13}\text{C}_3]$ 1-hydroxy-2-methyl-2-butenyl 4-diphosphate

Example 19

Detection of phosphorylated metabolites of the mevalonate-independent pathway

Method A) By a TLC method

Aliquots (10 μ l) of the cell-free extracts from recombinant cells prepared as described above (see example 16) are spotted on a Polygram® SIL NH-R thin layer plate (Macherey-Nagel, Düren, Germany). The TLC plate is then developed in a solvent system of n-propanol: ethyl acetate: water, 6:1:3 (v/v/v). The running time is about 4 h. The radio chromatogram is monitored and evaluated by a Phosphor Imager (Storm 860, Molecular Dynamics, USA). The R_f -values of the compounds under study are shown in Table 4.

Table 4: R_f -values of precursors and intermediates of the mevalonate-independent terpenoid pathway

Chemical compound	R_f -value
1-deoxy-D-xylulose	0.80
1-deoxy-D-xylulose 5-phosphate	0.5
2C-methyl-D-erythritol 4-phosphate	0.42
4-diphosphocytidyl-2C-methyl-D-erythritol	0.33
4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate	0.27
2C-methyl-D-erythritol 2,4-cyclodiphosphate	0.47
1-hydroxy-2-methyl-2-butenyl 4-diphosphate	0.17

Method B) By a HPLC method

Aliquots (100 μ l) of the cell-free extracts from recombinant cells prepared as described above (see example 16), are analyzed by HPLC using a column of Multospher 120 RP 18-AQ-5 (4.6 x 250 mm, particle size 5 μ m, CS-Chromatographic Service GmbH, Langerwehe, Germany) that has been equilibrated for 15 min with 10 mM tetrabutylammonium hydrogensulfate (TBAS), pH 6.0, at a flow rate of 0.75 ml min⁻¹. After injection of the sample, the column is developed for 20 min with 10 mM TBAS, then for 60 min with a linear gradient of 0 - 42 % (v/v)

methanol in 10 mM TBAS. The effluent is monitored by a continuous-flow radio detector (Beta-RAM, Biostep GmbH, Jahnndorf, Germany). The retention volumes of the compounds under study are shown in Table 5.

Table 5: Retention volumes of precursors and intermediates of the mevalonate-independent terpenoid pathway

Chemical compound	Retention volume [ml]
1-deoxy-D-xylulose	6.0
1-deoxy-D-xylulose 5-phosphate	15
2C-methyl-D-erythritol 4-phosphate	13.5
4-diphosphocytidyl-2C-methyl-D-erythritol	30.8
4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate	41.3
2C-methyl-D-erythritol 2,4-cyclodiphosphate	31.5
1-hydroxy-2-methyl-2-butenyl 4-diphosphate	42.8

Example 20

Purification of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate

The crude cell free extract obtained from the feeding experiment with recombinant *Escherichia coli* XL1-pBS_{Scyclo}-pACYCgcpE using [2-¹⁴C]- and [U-¹³C₅]1-deoxy-D-xylulose (see example 16) is lyophilized. The residue is dissolved in 600 µl of water and centrifuged for 10 min at 14,000 ppm. Aliquots of 90 µl are applied on a column of Nucleosil 10 SB (4.6 x 250 mm, Macherey & Nagel, Düren, Germany) which is developed with a linear gradient of 0.1 - 0.25 M ammonium formate in 70 ml at a flow rate of 2 ml min⁻¹. The retention volumes for 2C-methyl-D-erythritol-2,4-cyclodiphosphate and 1-hydroxy-2-methyl-2-butenyl 4-diphosphate are 25 and 44 ml, respectively. Fractions are collected and lyophilized. NMR data of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate are identical with the data shown in example 18, Table 2.

Example 21

Construction of a vector carrying the *xylB*, *dxr*, *ispD*, *ispE*, *ispF* and *ispG* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXP reductoisomerase, CDP-

ME synthase, CDP-ME kinase cMEPP synthase and 1-hydroxy-2-methyl-2-butenyl 4-diphosphate synthase

The *E. coli* ORF *ispG* (accession no. gb AE000338) from base pair (bp) position 372 to 1204 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-GCGGGAGACCGCGGGAGAGAAATTAACCATGCATAACCAGGCTCCAATTGCG-3', 10 pmol of the primer 5'-CGCTTCCCAGCGGCCGCTTATTTTCAACCTGCTGAACG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplicate is purified with the PCR purification kit from Qiagen (Hilden).

1.4 µg of the vector pBScyclo (Example 5) and 0.8 µg of the purified PCR product are digested with *Sac*II and *Nof*I in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 18 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBScyclogcpE. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBScyclogcpE is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBScyclogcpE is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000338). The DNA sequence of

the vector construct pBScyclogcpE is shown in Annex H.

Example 22

Construction of a vector carrying the *xylB*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG* and *lytB* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXR reductoisomerase, CDP-ME synthase, CDP-ME kinase, cMEPP synthase, 1-hydroxy-2-methyl-2-butenyl 4-diphosphate synthase and LytB

The *E. coli* ORF *lytB* (accession no. gb AE005179) from base pair (bp) position 7504 to 8454 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5' - AAATCGGAGCTCGAGGAGAAATTAACCATGCAGATCCTGTTGGCC-3', 10 pmol of the primer 5'-GCTGCTCCGCGTTAATCGACTTCACGAATATCG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

1.3 µg of the vector pBScyclogcpE (Example 21) and 0.7 µg of the purified PCR product are digested with SacI and SacII in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 16 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBScyclogcpElytB. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBScyclogcpElytB is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBScyclogcpElytB is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE005179).

Example 23

Incorporation experiment with recombinant *Escherichia coli* XL1-pBScyclogcpE using [U-¹³C₅]1-deoxy-D-xylulose

0.1 litre of Terrific Broth (TB) medium containing 18 mg of ampicillin are inoculated with *E. coli* strain XL1-Blue harbouring the plasmid pBScyclogcpE. The cells are grown in a shaking culture at 37 °C overnight. At an optical density (600 nm) of 4.8 – 5.0, 30 mg (0.1 mmol) of cytidine are added. A solution containing 1.2 g of lithium lactate (12.5 mmol), 6 ml of crude [U-¹³C₅]1-deoxy-D-xylulose (0.05 mmol) (see examples 8, 9 and 10) in 0.1 M Tris hydrochloride (pH=7.5) at a final volume of 30 ml are added continuously within 2 hours. Aliquots of 25 ml are taken at time intervals of 1 h and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 µl of 20 mM NaF in D₂O or in 700 µl of a mixture of methanol and D₂O (6:4, v/v) containing 10 mM NaF, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the cell free extracts are recorded directly with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). In order to avoid degradation during work-up, the structures of the products are determined by NMR spectroscopy without further purification.

The relative amount of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate to 2C-methyl-D-erythritol 2,4-cyclodiphosphate could be raised by a factor of approximately 2-3 by the addition of lithium lactate to the medium.

Example 24

Preparation of (E)-1-hydroxy-2-methyl-2-butenyl diphosphate triammonium salt (8)

General. Chemicals are obtained from Acros Organics (Fisher Scientific GmbH, Schwerte, Germany), SIGMA-ALDRICH (Deisenhofen, Germany), MERCK (Darmstadt, Germany) and used without further purification. Solvents are used distilled and/or dried. Chromatography is performed on silica gel 60 (230-400 mesh, Fluka Riedel-de Haen, Taufkirchen, Germany), DOWEX 50 WX8 (200-400 mesh, SERVA, Heidelberg, Germany), and Cellulose (Avicel, Cellulose mikrokristallin, Merck, Darmstadt, Germany). TLC is performed on silica gel 60 F₂₅₄ plastic sheets (MERCK) or cellulose F plastic sheets (MERCK), detection by anisaldehyde solution (anisaldehyde:H₂SO₄:HAc 0.5:1:50 v/v/v). NMR-spectra are recorded on BRUKER AMX 400, DRX 500, and AC 250 spectrometer at room temperature.

Acetonyl tetrahydropyranyl ether (12) (Hagiwara *et al.*, 1984).

A mixture of 339 mg (1.35 mmol) of pyridinium-toluene-4-sulfonate, 9.35 ml (10.0 g, 0.135 mol) of hydroxyacetone, and 24.7 ml (22.7 g, 0.270 mol) of 3,4-dihydro-2H-pyran is stirred at room temperature for 2.5 h. Residual 3,4-dihydro-2H-pyran is removed under reduced pressure. The crude mixture is purified by FC on silicagel (hexanes/acetone 4:1, 6.5 × 20 cm) to yield 18.7 g (0.118 mol, 88%) of a colorless liquid.

¹H NMR (CDCl₃, 500 MHz) δ 4.62 (t, J = 3.6 Hz, 1H), 4.22 (d, J = 17.3 Hz, 1H), 4.09 (d, J = 17.3 Hz, 1H), 3.83-3.79 (m, 1H), 3.51-3.47 (m, 1H), 2.15 (s, 3H), 1.87-1.49 (m, 6H); ¹³C NMR (CDCl₃, 126 MHz) δ 206.7, 98.7, 72.3, 62.3, 30.2, 26.5, 25.2, 19.2; MS (CI, isobutane) *m/z* 159 [M + 1]⁺.

(E,Z)-Ethyl-2-methyl-1-tetrahydropyranyloxy-but-2-enoate (13) (Watanabe *et al.*, 1996).

33.0 g (94.8 mmol) of (ethoxycarbonylmethylen)-triphenylphosphorane are dissolved in 500 ml of dry toluene under nitrogen atmosphere at room temperature. Then, 10.0 g (63.2 mmol) of acetonyl tetrahydropyranyl ether **12** are added and the mixture is heated to reflux. After 39 h at this temperature the solvent is evaporated *under reduced pressure* to yield an orange oil. Major amounts of triphenylphosphin oxide are precipitated by the addition of 100 ml hexanes/acetone 9:1. After filtration the filtrate is concentrated and another 100 ml of hexanes/acetone 9:1 are added. The solid is filtered off and the solvent removed to yield 18 g of an orange oil that is purified by FC on silicagel (hexanes/acetone 9:1, 6.5 × 28 cm) to yield 12.9 g (56.5 mmol, 89%) of a mixture of (E)-**13**/(Z)-**13** = 5:1.

(E)-**13**. ¹H NMR (CDCl₃, 500 MHz) δ 5.96 (q, J = 1.4 Hz, 1H), 4.62 (t, J = 3.5 Hz, 1H), 4.20 (dd, J = 15.5 Hz, 1.3 Hz, 1H), 4.14 (q, J = 7.1 Hz, 2H), 3.93 (dd, J = 15.6, 1.3 Hz, 1H), 3.84-

3.79 (m, 1H), 3.52-3.48 (m, 1H), 2.08 (d, $J = 1.4$ Hz, 3H), 1.88-1.50 (m, 6H), 1.26 (t, $J = 7.1$ Hz, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 166.8, 154.7, 114.5, 98.0, 70.6, 62.0, 59.7, 30.3, 25.3, 19.1, 15.9, 14.3; MS (CI, isobutane) m/z 229 $[\text{M} + 1]^+$.

(Z)-(13). ^1H NMR (CDCl_3 , 500 MHz) δ 5.71 (q, $J = 1.4$ Hz, 1H), 4.60 (t, $J = 3.6$ Hz, 1H), 4.20 (dd, $J = 15.5$ Hz, 1.3 Hz, 1H), 4.11 (q, $J = 7.1$ Hz, 2H), 3.93 (dd, $J = 15.6$, 1.3 Hz, 1H), 3.84-3.79 (m, 1H), 3.52-3.48 (m, 1H), 1.97 (d, $J = 1.4$ Hz, 3H), 1.88-1.50 (m, 6H), 1.24 (t, $J = 7.1$ Hz, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 165.9, 156.8, 116.9, 98.7, 66.5, 62.3, 59.8, 30.6, 25.3, 21.9, 19.5, 14.3; MS (CI, isobutane) m/z 229 $[\text{M} + 1]^+$.

(E,Z)-2-Methyl 1-tetrahydropyranyloxy-but-2-ene-4-ol (14) (Watanabe *et al.*, 1996).

A solution of ester 13 (8.73 g, 38.2 mmol) in 100 ml of dry CH_2Cl_2 is cooled to -78°C . Then, 91.8 ml (91.8 mmol) of 1.0 M DIBAH in hexanes are added slowly under an atmosphere of nitrogen. The resulting solution is stirred for 3 h at -78°C before the reaction is quenched by the addition of 1.5 ml of 1 M NaOH. After warming to room temperature the solvent is removed *under reduced pressure*. The resulting gummy residue is widely dissolved by adding twice 100 ml of MeOH. The resulting mixture is passed through a column of SiO_2 , evaporated from the solvent and then loaded on a column of $\text{SiO}_2/\text{Na}_2\text{SO}_4$ that is purged with 1400 ml of MeOH. Evaporation of the solvent gives 9.5 g of a colorless liquid that is purified by FC on silica gel (hexanes/acetone 1:3, 6.5×16 cm) to yield 6.98 g (37.4 mmol, 98%) of a colorless liquid **(E)-14/(Z)-14 = 6:1**.

(E)-(14). ^1H NMR (CDCl_3 , 500 MHz) δ 5.68 (tq, $J = 6.6$, 1.3 Hz, 1H), 4.60 (t, $J = 3.6$ Hz, 1H), 4.20 (d, $J = 6.8$ Hz, 2H), 4.12 (d, $J = 12.0$ Hz, 1H), 3.87-3.82 (m, 1H), 3.85 (d, $J = 12.5$ Hz, 1H), 3.52-3.48 (m, 1H), 1.86-1.48 (m, 6H), 1.69 (s, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 135.7, 125.4, 97.8, 71.9, 62.1, 59.1, 30.5, 25.4, 19.4, 14.1; MS (CI, isobutane) m/z 169 $[\text{M} - \text{H}_2\text{O} + 1]^+$.

(Z)-(14). ^1H NMR (CDCl_3 , 500 MHz) δ 5.64 (tq, $J = 6.6$, 1.3 Hz, 1H), 4.63 (t, $J = 3.3$ Hz, 1H), 4.20 (d, $J = 6.8$ Hz, 2H), 4.15 (d, $J = 11.8$ Hz, 1H), 3.87-3.82 (m, 1H), 3.83 (d, $J = 11.3$ Hz, 1H), 3.52-3.48 (m, 1H), 1.86-1.48 (m, 6H), 1.79 (s, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 136.2, 128.6, 96.6, 65.1, 61.8, 58.1, 30.3, 25.3, 21.9, 19.0; MS (CI, isobutane) m/z 169 $[\text{M} - \text{H}_2\text{O} + 1]^+$.

(E,Z)-4-Chloro-2-methyl 1-tetrahydropyranyloxy-but-2-en (15) (Hwang *et al.*, 1984).

To a solution of alcohol 14 (1.00 g, 5.37 mmol) in 10 ml of dry CH_2Cl_2 are added 918 mg (7.52 mmol) of DMAP in 10 ml of dry CH_2Cl_2 and 1.23 g (6.44 mmol) of *p*-TsCl in 10 ml of dry

CH_2Cl_2 . The resulting solution is stirred at room temperature for 1 h. After evaporation of the solvent *under reduced pressure* the residue is purified by FC on silica gel (CH_2Cl_2 , 5×20 cm) to obtain 693 mg (3.39 mmol, 63%) of a colorless liquid (E)-15/(Z)-15 = 6:1.

(E)-15. ^1H NMR (CDCl_3 , 500 MHz) δ 5.77 (tq, $J = 8.0$, 1.5 Hz, 1H), 4.64 (t, $J = 3.6$ Hz, 1H), 4.18 (d, $J = 12.8$ Hz, 1H), 4.15 (d, $J = 8.0$ Hz, 2H), 3.92 (d, $J = 12.8$ Hz, 1H), 3.90-3.86 (m, 1H), 3.59-3.52 (m, 1H), 1.92-1.52 (m, 6H), 1.77 (s, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 138.6, 121.7, 97.8, 71.3, 62.1, 40.2, 30.5, 25.4, 19.3, 13.9; MS (Cl, isobutane) m/z 205 [$M + 1$] $^+$.

(Z)-15. ^1H NMR (CDCl_3 , 500 MHz) δ 5.65 (t, $J = 8.1$ Hz, 1H), 4.61 (t, $J = 3.6$ Hz, 1H), 4.18 (d, $J = 12.8$ Hz, 1H), 4.15 (d, $J = 8.0$ Hz, 2H), 3.92 (d, $J = 12.8$ Hz, 1H), 3.90-3.86 (m, 1H), 3.59-3.52 (m, 1H), 1.92-1.52 (m, 6H), 1.86 (s, 3H); ^{13}C NMR (CDCl_3 , 126 MHz) δ 138.3, 124.6, 97.5, 64.7, 62.2, 40.1, 30.5, 25.4, 21.8, 19.4; MS (Cl, isobutane) m/z 205 [$M + 1$] $^+$.

(E,Z)-2-Methyl 1-tetrahydropyranyloxy-but-2-enyl diphosphate triammonium salt (16)
(Davisson *et al.*, 1986).

To a solution of chloride 15 (260 mg, 1.27 mmol) in 1.3 ml of MeCN a solution of 1.38 g (1.52 mmol) tris(tetra-*n*-butylammonium) hydrogen pyrophosphate in 3.0 ml of MeCN is added slowly at room temperature, obtaining an orange-red solution. The reaction is followed by ^1H -NMR, taking advantage of the up field shift of the multiplet of H-3. After 2 h the reaction is finished and the solvent removed *under reduced pressure*. The orange oil is dissolved in 2.5 ml of H_2O and passed through a column of DOWEX 50 WX8 (2.5×3 cm) cation-exchange resin (NH_4^+ form) that has been equilibrated with two column volumes (40 ml) of 25 mM NH_4HCO_3 . The column is eluted with 60 ml of 25 mM NH_4HCO_3 . The resulting solution is lyophilized, dissolved in 5 ml of isopropanol/100 mM NH_4HCO_3 1:1 and loaded on a cellulose column (2×18 cm) that is eluted by isopropanol/100 mM NH_4HCO_3 1:1. The effluent is lyophilized obtaining 495 mg (1.25 mmol, 98%) of (E)-16/(Z)-16 = 6:1 as a white solid.

(E)-16. ^1H NMR (D_2O , 500 MHz) δ 5.52 (tq, $J = 6.8$ Hz, 1H), 4.65 (s, 1H), 4.34 (t, $J = 7.0$ Hz, 2H), 3.98 (d, $J = 12.3$ Hz, 1H), 3.84 (d, $J = 12.1$ Hz, 1H), 3.74-3.70 (m, 1H), 3.42-3.38 (m, 1H), 1.61-1.57 (m, 2H), 1.54 (s, 3H), 1.40-1.32 (m, 4H); ^{13}C NMR (D_2O , 126 MHz) δ 136.4, 123.9 (dd, $J = 8.0$, 2.3 Hz), 98.5, 72.5, 63.2, 62.2 (d, $J = 5.3$ Hz), 29.9, 24.5, 19.0, 13.4; ^{31}P NMR (D_2O , 101 MHz) δ -5.62 (d, $J = 20.9$ Hz), -7.57 (d, $J = 20.8$ Hz).

(Z)-16. ^1H NMR (D_2O , 500 MHz) δ 5.52 (t, $J = 6.8$, 1H), 4.65 (s, 1H), 4.31 (t, $J = 7.1$ Hz, 2H), 3.98 (d, $J = 12.3$ Hz, 1H), 3.84 (d, $J = 12.1$ Hz, 1H), 3.74-3.70 (m, 1H), 3.42-3.38 (m, 1H), 1.64

(s, 3H), 1.61-1.57 (m, 2H), 1.40-1.32 (m, 4H); ^{13}C NMR (D_2O , 126 MHz) δ 136.3, 125.8 (d, J = 8.6 Hz), 98.6, 72.5, 63.2, 61.8 (d, J = 5.1 Hz), 29.9, 24.5, 20.8, 19.0; ^{31}P NMR (D_2O , 101 MHz) δ -5.69 (d, J = 20.8 Hz), -7.68 (d, J = 20.8 Hz).

(E,Z)-1-Hydroxy-2-methyl-but-2-enyl diphosphate triammonium salt (8) (Davisson *et al.*, 1986).

268 mg (0.675 mmol) of protected pyrophosphate **16** are dissolved in 2.0 ml of D_2O and the pH is adjusted to 1 by addition of 40 μl of 37% DCl in D_2O . After 1 min at this pH the solution is neutralized by addition of 40 μl of 40% NaOD in D_2O and an ^1H NMR is measured that demonstrated 50% deprotection. The procedure is repeated until deprotection is finished and just small amounts of decomposition product are formed to get in total 7 min at pH 1. Purification is performed by loading the neutral solution that is diluted by addition of 2 ml of isopropanol/100 mM NH_4HCO_3 1:1 on a cellulose column (isopropanol/100 mM NH_4HCO_3 1:1, 2×10.5 cm) to yield 193 mg (0.616 mmol, 91%) of a white solid of (E)-8/(Z)-8 = 7:1.

(E)-8. ^1H NMR (D_2O , 500 MHz) δ 5.51 (tq, J = 6.8, 1.2 Hz, 1H), 4.41 (t, J = 7.2 Hz, 2H), 3.90 (s, 2H), 1.59 (s, 3H); ^{13}C NMR (D_2O , 126 MHz) δ 139.8, 120.6 (d, J = 7.7 Hz), 66.5, 62.4 (d, J = 5.3 Hz), 13.2; ^{31}P NMR (D_2O , 101 MHz) δ -4.48 (d, J = 20.8 Hz), -7.06 (d, J = 20.8 Hz).

(Z)-8. ^1H NMR (D_2O , 500 MHz) δ 5.49 (tm, J = 6.8 Hz, 1H), 4.41 (t, J = 7.3 Hz, 2H), 4.03 (s, 2H), 1.70 (s, 3H); ^{13}C NMR (D_2O , 126 MHz) δ 139.8, 123.5 (d, J = 7.7 Hz), 61.7 (d, J = 5.1 Hz), 59.9, 20.6; ^{31}P NMR (D_2O , 101 MHz) δ -4.48 (d, J = 20.8 Hz), -7.06 (d, J = 20.8 Hz).

Reagents and conditions (steps (a) to (f) in Fig. 4: 1): (a) DHP, PPTS, 25 $^\circ\text{C}$ (2.5 h); (b) $\text{Ph}_3\text{PCHCO}_2\text{Et}$, toluene, reflux (39 h); (c) (1) DIBAL, CH_2Cl_2 , -78 $^\circ\text{C}$ (3 h), (2) 1 M NaOH/ H_2O ; (d) *p*-TsCl, DMAP, CH_2Cl_2 , 25 $^\circ\text{C}$ (1 h); (e) $((\text{CH}_3\text{CH}_2\text{CH}_2\text{CH}_2)_3\text{N})_3\text{HP}_2\text{O}_7$, MeCN, 25 $^\circ\text{C}$ (2 h); (f), HCl/ H_2O pH 1, 25 $^\circ\text{C}$ (7 min).

Example 25

Identification of (E)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate

The structure of the GcpE product is further analyzed by comparison with the chemical shifts of a synthetic sample of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate.

For this purpose, [2-¹⁴C]1-hydroxy-2-methyl-2-(*E*)-butenyl 4-diphosphate (0.36 μ Ci) is added to a cell extract obtained from bioengineered *Escherichia coli* cells endowed with artificial gene constructs expressing *xyfB*, *ispC*, *ispD*, *ispE*, *ispF* and *gcpE* gene which are supplied with [U-¹³C]₅-1-deoxy-D-xylulose (see example 16). The supernatant of the cell extract is purified by HPLC (Nucleosil 5 SB, 7.5 \times 250 mm, developed with a gradient of 100 mM to 250 mM NH₄HCOO, flow rate 2 ml/min, 35 min). The product is eluted at 23 min and collected. After lyophilization the residue is dissolved in D₂O (pH 6) and subjected to ¹H NMR analysis (Figure 3-A).

Then, 40 μ l of a solution of synthetically prepared (E,Z)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate (E/Z = 7:1) (D₂O, pH 7) are added to the NMR sample and again analyzed by ¹H NMR spectroscopy (Figure 3-B). On the one hand, as shown in Figure 3-B, signals accounting for (E)-1-hydroxy-2-methyl-2-butenyl are selectively increased, providing evidence that the biologically produced structure is identical with the synthetically produced one, i.e. the (E)-isomer. On the other hand, the minor (Z)-isomer raises without any correlation to signals of the biologically afforded product. Figure 3-C shows the same effects after addition of another 40 μ l of solution of the synthetically prepared (E,Z)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate.

Example 26

Incorporation of (E)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate into the lipid soluble fraction of *Capsicum annuum* chromoplasts.

Chromoplasts are isolated by a slight modification of a method described by Camara (Camara, 1985; Camara, 1993). Pericarp of red pepper (650 g) is homogenized at 4 °C in 600 ml of 50 mM Hepes, pH 8.0, containing 1 mM DTE, 1 mM EDTA and 0.4 M sucrose (buffer A). The suspension is filtered through four layers of nylon cloth (50 μ m) and centrifuged (10 min, 4,500 rpm, GSA rotor) to obtain a pellet of crude chromoplasts which is homogenized in 200 ml of buffer A. The suspension is centrifuged (10 min, 4,500 rpm, GSA rotor). The pellet is homogenized and resuspended in 3 ml of 50 mM Hepes, pH 7.6, containing 1 mM DTE. The suspension is filtered through one layer of nylon cloth (50 μ m).

Reaction mixtures contain 100 mM Hepes, pH 7.6, 2 mM MnCl₂, 10 mM MgCl₂, 5 mM NaF, 2 mM NADP⁺, 1 mM NADPH, 6 mM ATP, 20 μ M FAD and 2 mg of chromoplasts. 8.8 nmol of [2-¹⁴C]2C-methyl-D-erythritol 2,4-cyclodiphosphate, [2-¹⁴C]1-hydroxy-2-methyl-2-(*E*)-butenyl diphosphate or [2-¹⁴C]isopentenyl diphosphate (specific concentrations 15.8 μ Ci/ μ mol) are

added and the mixtures are incubated at 30 °C overnight. The reaction is terminated by methylene chloride extraction. The organic phase is concentrated under a stream of nitrogen. Aliquots are spotted on silica gel plates (Polygram SIL-G, UV254, Macherey-Nagel, Düren, Germany). The plates are developed with hexane : ether = 6: 1 (system I) and/or hexane : toluene = 9 : 1 (system II), respectively. The chromatograms are monitored with a phosphor imager (Storm 860, Molecular dynamics, Sunnyvale, CA, USA). The R_f -values of geranylgeraniol and the carotene fraction in system I are 0.35 and 0.9, respectively. The R_f -values of β -carotene, phytoene and phytofluene in system II are 0.65, 0.60 and 0.55, respectively.

The evaluation of the chromatograms show that radioactivity can be efficiently diverted from 1-hydroxy-2-methyl-2-(*E*)-butenyl diphosphate into the geranylgeraniol, β -carotene, phytoene and phytofluene fractions of *C. annuum* chromoplasts establishing 1-hydroxy-2-methyl-2-(*E*)-butenyl diphosphate as a real intermediate of the non-mevalonate pathway downstream from 2C-methyl-D-erythritol 2,4-cyclodiphosphate and upstream from isopentenyl diphosphate.

Example 27

Construction of a vector carrying the *ispG* (*gcpE*) and *ispH* (*lytB*) genes of *Escherichia coli* capable for transcription and expression thereof

The *E. coli* ORF *ispH* (*lytB*) (accession no. gb AE000113) from base pair (bp) position 5618 to 6568 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-GCTTGCCTCGACGAGGAGAAATTAAACCATGCAGATCCTGTTGGCCACC-3', 10 pmol of the primer 5'-GCTGCTCGGCCGTTAATCGACTTCACGAATATCG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 μ l containing 1.5 mM $MgCl_2$, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 μ l is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.4 µg of the vector pACYC184 (Chang and Cohen 1978, NEB) and 0.7 µg of the purified PCR product are digested with *Sall* and *EagI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 18 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYClytB. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYClytB is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYClytB is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000113).

The *E. coli* ORF *ispG* (*gcpE*) (accession no. gb AE000338) from base pair (bp) position 372 to 1204 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-CGTACCGGATCCGAGGAGAAATTAACCATGCATAACCAGGCTCCAATTC-3', 10 pmol of the primer 5'-CCCATCGTCGACTTATTTTCAACCTGCTGAACGTC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.0 µg of the vector pACYClytB and 0.9 µg of the purified PCR product are digested with *Bam*HI and *Sall* in order to produce DNA fragments with overlapping ends. The restriction

mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 23 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYClytBgcpE. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYClytBgcpE is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYClytBgcpE is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000338).

The DNA sequence of the vector construct pACYClytBgcpE is shown in Annex I.

The DNA and corresponding amino acid sequence of *ispH* (*lytB*) from *Escherichia coli* is shown in Annex J.

Example 28

Construction of a vector carrying the *xylB*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG* and *ispH* genes of *Escherichia coli* capable for transcription and expression of D-xylulokinase, DXP reductoisomerase, CDP-ME synthase, CDP-ME kinase cMEPP synthase, 1-hydroxy-2-methyl-2-butenyl 4-diphosphate synthase and IPP/DMAPP synthase

The *E. coli* ORFs *ispG* (formerly *gcpE*) and *ispH* (formerly *lytB*) are amplified by PCR using the plasmid pACYClytBgcpE (see example 27) as template. The reaction mixture contains 10 pmol of the primer 5'-AGGCTGGCGGCCGCTTAATCGACTTCACGAATATCG-3', 2 ng of pACYCgcpElytB DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 150 sec at 72 °C followed. After further incubation for 20 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplicate is purified with the PCR purification kit from Qiagen (Hilden).

1.7 µg of the vector pBScyclo (Example 5) and 1.3 µg of the purified PCR product are digested with *SacII* and *NotI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

22 ng of the purified vector DNA and 19 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pBScyclogcpElytB2. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pBScyclogcpElytB2 is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pBScyclogcpElytB2 is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. The DNA sequence of the vector construct pBScyclogcpElytB2 is shown in Annex K.

Example 29

Incorporation experiment with recombinant *Escherichia coli* XL1-pBScyclogcpElytB2 using [U-¹³C₅]1-deoxy-D-xylulose

0.1 litre of Terrific Broth (TB) medium containing 18 mg of ampicillin are inoculated with *E. coli* strain X11-Blue harbouring the plasmid pBScyclogcpElytB2. The cells are grown in a shaking culture at 37 °C for overnight. At an optical density (600 nm) of 1.3-1.7 a solution containing 2.4 g of lithium lactate (25 mmol), 10 ml of crude [U-¹³C₅]1-deoxy-D-xylulose (0.05 mmol) (see example 8) at a final volume of 30 ml (pH=7.4) are added continuously within 2 hours. Aliquots

of 40 ml are taken at time intervals of 30 minutes and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 ml of a mixture of methanol and D₂O (6:4, v/v) containing 10 mM NaF, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the cell free extracts are recorded directly with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). In order to avoid degradation during work-up, the structures of the products are determined by NMR spectroscopy without further purification.

Example 30

Structure determination of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP)

The ¹H-decoupled ¹³C NMR spectrum using [U-¹³C₅]1-deoxy-D-xylulose as starting material (see examples 8 and 30) displays five intense ¹C-¹³C coupled signals belonging to 2C-methyl-D-erythritol 2,4-cyclodiphosphate (Herz et al., 2000) and five ¹³C-¹³C coupled signals with low intensities belonging to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate (see example 18) (100:3 ratio for the 2-methyl ¹³C NMR signal intensities of 2C-methyl-D-erythritol 2,4-cyclodiphosphate and 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, respectively).

In addition a set of , five ¹³C-¹³C coupled signals at 21.6 (doublet), 37.8 (triplet), 64.1 (doublet), 111.6 (doublet), and 143.3 ppm (doublet of triplets) (unknown metabolite A) accompanied by signals at 21.1 (doublet), 39.6 (triplet), 59.3 (doublet), 111.8 (doublet), and 143.2 ppm (doublet of triplets) (unknown metabolite B) is detected. The ratio of the 2-methyl signal of 2C-methyl-D-erythritol 2,4-cyclodiphosphate and the putative methyl signals of the unknown compounds at 21.6 ppm (metabolite A) and 21.1 ppm (metabolite B) is 100:24:4, respectively.

Moreover, ¹³C coupled signals with low intensities belonging to another unknown compound (metabolite C) at 17.1 (doublet), 24.9 (doublet), 62.7 (doublet), 119.6 (double-doublet) and 139.4 ppm (multiplet) are detected. The ratio of the intensities of the putative methyl signals at 21.6 (metabolite A), 17.1 and 24.9 (metabolite C) is 100:13:13, respectively.

The ³¹P NMR spectrum of the reaction mixture is characterized by intense signals for 2C-

methyl-D-erythritol 2,4-cyclodiphosphate (Herz et al., 2000). Furthermore, ^{31}P - ^{31}P coupled broadened signals are observed at a chemical shift range typical for organic diphosphates (-6 to -13 ppm, ^{31}P - ^{31}P coupling constants, 20 Hz).

Metabolite A:

The signals of metabolite A at 111.6 and 143.3 ppm are conducive of a double bond motif, and the signals at 64.1, 37.8 and 21.6 ppm reflect three aliphatic carbon atoms one of which (signal at 64.1 ppm) appears to be connected to OH or OR (R=unknown).

Additional information about the structure of the unknown metabolite A can be gleaned from the ^{13}C coupling pattern. Three of the ^{13}C NMR signals (21.6, 64.1 and 111.6 ppm) are split into doublets indicating three ^{13}C atoms each connected to only one ^{13}C -labelled neighbour, one signal (37.8 ppm) displays a pseudo-triplet signature indicating a ^{13}C atom with two adjacent ^{13}C atoms, and one signal (143.3 ppm) is split into a doublet of triplets indicating a ^{13}C atom with three ^{13}C connections. In conjunction with the chemical shifts, this connectivity pattern establish metabolite A as an isopentenyl derivative.

The complex signature for the signal at 143.3 ppm deserves a more detailed analysis. The large coupling (71 Hz) is typical for ^{13}C - ^{13}C couplings between carbon atoms involved in carbon-carbon double bonds. A 71 Hz coupling is also found for the doublet signal at 111.6 ppm representing the second carbon of the double bond. Due to the coupling pattern and the chemical shifts the presence of an exo-methylene function is obvious. The two additional ^{13}C couplings found in the triplet substructure of the signal at 143.3 ppm are both 41 Hz, and establish the respective carbon as the branching point of the structure.

HMQC experiments reveal the ^1H NMR chemical shifts, as well as ^{13}C - ^1H and ^1H - ^1H spin systems. More specifically, the ^{13}C NMR signal at 111.6 ppm correlates to a ^1H NMR signal at 4.73 ppm, whereas the signal at 143.3 ppm gives no ^{13}C - ^1H correlation. The signals at 64.1, 37.8, and 21.6 ppm give ^{13}C - ^1H correlations to ^1H -signals at 4.00, 2.31, and 1.68 ppm, respectively. As shown by HMQC-TOCSY experiments, the proton signals at 2.31 and 4.00 are coupled, whereas the signals at 4.73 and 1.68 ppm are found as singlets in the HMQC-TOCSY experiment. The observed ^1H NMR chemical shifts in combination with the coupling patterns demonstrate that Metabolite A is an isopentenyl derivative with a single bonded heteroatom (most plausibly O) at position 1.

The ^{31}C and ^1H chemical shifts of an authentic sample of isopentenyl diphosphate (IPP, measured in the same solvent mixture) are identical to the chemical shifts assigned to

metabolite A. Thus, metabolite A is identified as $[U-^{13}C_3]$ IPP.

Metabolite B:

As noted above, the coupling and correlation pattern of metabolite B observed in the ^{13}C NMR signals, as well as in the HMQC and HMQC-TOCSY spectra, is virtually the same as for metabolite A (IPP) suggesting that the carbon connectivities of metabolite B and IPP are identical. As the most significant difference between the NMR data of metabolite B and IPP the ^{13}C NMR chemical shift of one doublet signal for metabolite B (59.3 ppm) corresponding to the C-1 signal of IPP (64.1 ppm) is upfield shifted by 4.9 ppm. This suggests that a phosphate moiety is missing at C-1 in metabolite B. Therefore, metabolite B is assigned as $[U-^{13}C_3]$ isopentene-1-ol. Presumably, isopentene-1-ol is formed from IPP by the catalytic action of pyrophosphatases and phosphatases present in the experimental system.

Metabolite C:

As described above for metabolite A (IPP), the structure of metabolite C is assigned by NMR analysis. The ^{13}C coupling pattern of the signals attributed to metabolite C (three doublets, one double-doublet, one multiplet) suggests that the compound is another isopentane derivative. The chemical shifts observed for the double-doublet (119.6 ppm) and the multiplet (139.4 ppm) show that a carbon-carbon double bond connects C-2 (coupled to two ^{13}C neighbours) and C-3 (coupled to three ^{13}C neighbours) of the molecule.

The 1H NMR chemical shifts of metabolite C are revealed by HMQC and HMQC-TOCSY experiments showing two singlets at 1.75 and 1.71 ppm, and a spin system comprising signals at 5.43 and 4.45 ppm. In conjunction with the chemical shifts, this correlation pattern shows that metabolite C is a dimethylallyl derivative.

The ^{13}C and 1H NMR chemical shifts of an authentic sample of dimethylallyl diphosphate (DMAPP) are identical to the chemical shifts of the signals attributed to metabolite C. This leaves no doubt that metabolite C is $[U-^{13}C_3]$ dimethylallyl diphosphate (DMAPP).

The NMR data of metabolite A (IPP) and metabolite C (DMAPP) are summarized in Tables 6 and 7.

Table 6. NMR data of isopentenyl diphosphate (IPP)

Position	Chemical shifts, ppm			Coupling constants, Hz				
	$^1\text{H}^a$	$^{13}\text{C}^b$	$^{31}\text{P}^c$	J_{PC}	J_{HH}	J_{PP}	J_{PH}	J_{CC}^d
1	4.00	64.1		4.9	6.6		6.6	34
2	2.31	37.8		8.0	6.7			40, 40
3		143.3						71, 41, 41
4	4.73	111.6						71
5	1.68	21.6						41
P			- 7.8			nd		
P			- 11.9			19.5		

^areferenced to external trimethylsilylpropane sulfonate.^breferenced to external trimethylsilylpropane sulfonate.^creferenced to external 85 % orthophosphoric acid.^dobserved with $[\text{U-}^{13}\text{C}_5]\text{IPP}$

Table 7. NMR data of dimethylallyl diphosphate (DMAPP)

Position	Chemical shifts, ppm			Coupling constants, Hz				
	$^1\text{H}^a$	$^{13}\text{C}^b$	$^{31}\text{P}^c$	J_{PC}	J_{HH}	J_{PP}	J_{PH}	J_{CC}^d
1	4.45	62.7		3.6	6.6		6.6	47
2	5.43	119.6		9.0	7.2			75, 48
3		139.4						nd
4	1.75	24.9						42
5	1.71	17.1						41
P			- 9.1			21.7		
P			- 6.4			21.5		

^areferenced to external trimethylsilylpropane sulfonate.^breferenced to external trimethylsilylpropane sulfonate.^creferenced to external 85 % orthophosphoric acid.^dobserved with $[\text{U-}^{13}\text{C}_5]\text{DMAPP}$

Example 31

Cloning of the *ispG* gene (fragment) from *Arabidopsis thaliana*

RNA is isolated from 1 g of 2 weeks old *Arabidopsis thaliana* var. Columbia plants (stems and leaves) by published procedures (Logemann et al. 1987).

A mixture containing 2.75 µg RNA, 50 nmol dNTP's, 1 µg random hexameric primer, 1 µg T₁₅ primer and 20 % first strand 5x buffer (Promega) in a total volume of 50 µl is incubated for 5 min. at 95 °C, cooled on ice and 500 U M-MLV reverse transcriptase (Promega) are added. The mixture is incubated for 1 h at 42 °C. After incubation at 92 °C for 5 min, RNase A (20 U) and RNase H (2 U) are added and the mixture is incubated for 30 min. at 37 °C.

The resulting cDNA (1 µl of this mixture) is used for the amplification of *ispG* by PCR.

The *A. thaliana* ORF *ispG* (accession no. dbj AB005246) without the coding region for the putative leader sequence from basepair (bp) position 2889 to 6476 is amplified by PCR using cDNA from *A. thaliana* as template. The reaction mixture contains 25 pmol of primer CCTGCATCCGAAGGAAGCCC, 25 pmol of primer CAGTTTTCAAAGAATGGCCC, 1 µl of cDNA, 2 U of Taq DNA polymerase (Eurogentec, Seraing, Belgium) and 20 nmol of dNTPs in a total volume of 100 µl in 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 95 °C. Then 40 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 20 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis. The PCR amplificate is purified with the PCR purification kit from Qiagen. 1.7 µg of purified PCR product are obtained.

The PCR amplificate is used as template for a second PCR reaction. The reaction mixture contains 25 pmol of primer TGAATCAGGATCCAAGACGGTGAGAAGG, 25 pmol of primer TCCGTTTGGTACCCTACTCATCAGCCACGG, 2 µl of the first PCR amplification, 2 U of Taq DNA polymerase (Eurogentec, Seraing, Belgium) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 95 °C. Then 40 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C follow. After further incubation for 20 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with PCR purification kit from Qiagen. 1.4 µg of purified PCR product are obtained. 2.0 µg of the vector pQE30 and 1.4 µg of the purified PCR product are digested with *Bam*HI and *Kpn*I in order to produce cohesive ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of vector DNA and 12 ng of PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pQEgcpEara. The ligation mixture is incubated over night at 4 °C. 2 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue and M15[pREP4] (Zamenhof *et al.*, 1972) cells. The plasmid pQEgcpEara is isolated as described above. 7 µg of plasmid DNA are obtained.

The DNA insert of the plasmid pQEgcpEara is sequenced as described above. The DNA sequence is found not to be identical with the sequence in the database (accession no. dbj AB005246, see Annex L).

Example 32

Screening of IspG (GcpE) enzyme activity

0.2 g cells of XL1-pACYClytBgcpE are suspended in 1 ml 50 mM Tris hydrochloride, pH 7.4 and 2 mM DTT, cooled on ice and sonified 3 × 7 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 80 % duty cycle output, control value of 4 output. The suspension is centrifuged at 14000 rpm for 15 minutes. The supernatant is used as crude cell extract in assays described as follows.

The assay mixture contains 100 mM Tris hydrochloride, pH 7.4, 1.2 mM dithiothreitol, 10 mM NaF, 1 mM CoCl₂, 2 mM NADH, 20 mM (18 µCi mol⁻¹) [2-¹⁴C]2C-methyl-erythritol 2,4-cyclodiphosphate, 0.5 mM pamidronate and 100 µl crude cell extract of XL1-pACYClytBgcpE in a total volume of 150 µl. The mixture is incubated for 10 to 45 min at 37 °C and cooled on ice. 10 µl of 30 % (g/v) trichloroacetic acid are added and the mixture is neutralized with 20 µl of 1 M NaOH. The mixture is centrifuged at 14.000 rpm for 10 minutes. Aliquotes of 130 µl of the supernatant are analyzed by reversed-phase ion-pair HPLC using a column of Multospher 120 RP 18-AQ-5 (4.6 × 250 mm, CS-Chromatographie Service GmbH, Langerwehe, Germany).

The column is developed with a linear gradient of 7-21 % (v/v) methanol in 20 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0 at a flow rate of 1 ml min⁻¹ and further with a linear gradient of 21-49 % (v/v) methanol in 15 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0. After washing the column with 49 % (v/v) methanol in 5 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0, the column is equilibrated with 7 % (v/v) methanol in 20 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0. The effluent is monitored by a continuous-flow radio detector (Beta-RAM, Biostep GmbH, Jahnsdorf, Germany). The retention volumes of 2C-methyl-erythritol 2,4-cyclodiphosphate, 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate, DMAPP/IPP are 18, 24 and 39 ml respectively.

After 10 minutes of incubation, about 13 % of 2C-methyl-erythritol 2,4-cyclodiphosphate have been converted into 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate (5 %) and into DMAPP/IPP (8 %), respectively.

After 45 min, no 1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate, but about 21 % of DMAPP/IPP was found in the assay mixture.

Example 33

Screening of Isph (LytB) activity

Assay mixtures contain 100 mM Tris hydrochloride, pH 7.4, 1.2 mM DTT, 10 mM NaF, 0.5 mM NADH, 60 µM FAD, 0.004 µM (18 µCi µmol⁻¹) [2-¹⁴C]1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate, 0.5 mM pamidronate (Dunford *et al.*, 2001) and 20 µl of crude cell extract of M15-pMALyB cells (prepared as described in example 2) in a total volume of 150 µl. The mixture is incubated for 30 min at 37 °C. The reaction is terminated by cooling on ice, addition of 10 µl of 30 % (g/v) trichloroacetic acid and immediate neutralization with 20 µl 1 M sodium hydroxide. The mixtures are centrifuged and aliquots (130 µl) of the supernatant are analyzed by reversed-phase ion-pair HPLC using a column of Multospher 120 RP 18-AQ-5 (4.6 x 250 mm, CS-Chromatographie Service GmbH, Langerwehe, Germany) analyzed by reversed-phase ion-pair HPLC using a column of Multospher 120 RP 18-AQ-5 (4.6 x 250 mm, CS-Chromatographie Service GmbH, Langerwehe, Germany). The column is developed with a linear gradient of 7-21 % (v/v) methanol in 20 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0 at a flow rate of 1 ml min⁻¹ and further with a linear gradient of 21-49 % (v/v) methanol in 15 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0. After

washing the column with 49 % (v/v) methanol in 5 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0, the column is equilibrated with 7 % (v/v) methanol in 20 ml of 10 mM tetra-n-butylammonium hydrogen phosphate, pH 6.0. The effluent is monitored by a continuous-flow radio detector (Beta-RAM, Biostep GmbH, Jahnsdorf, Germany).

Under standard assay conditions, the HPLC peak corresponding to the substrate 1-hydroxy-2-methyl-2-(*E*)-butenyl 4-diphosphate is completely diminished, whereas two new peaks corresponding to DMAPP and IPP appear, when crude cell extract of *E. coli* M15-pMAL1ytB cells is used as protein source. No conversion of 1-hydroxy-2-methyl-2-(*E*)-butenyl 4-diphosphate into DMAPP and IPP can be observed, when crude cell extract of *E. coli* wild-type is used as protein source. This findings clearly show that the FAD and NADH- or NADPH-dependent conversion of 1-hydroxy-2-methyl-2-(*E*)-butenyl 4-diphosphate into DMAPP and IPP is catalyzed by the recombinant LytB protein. The addition of pamidronate in the assay mixtures prevents a further metabolization of IPP and DMAPP by highly active prenyl transferases present in crude *E. coli* extracts and affects therefore the complete conversion of 1-hydroxy-2-methyl-2-(*E*)-butenyl 4-diphosphate into DMAPP and IPP.

Example 34

Construction of a vector carrying the *dxs*, *xyiB* and *ispC* genes capable for the transcription and expression thereof

The *B. subtilis* ORF *dxs* (accession no. dbj D84432) from base pair (bp) position 193991 to 195892 is amplified by PCR using pBSDXSBACSU plasmid DNA as template (see patent application PCT/EP00/07548). The reaction mixture contains 10 pmol of the primer 5'-GGCGACTCGCGAGAGGAGAAATTAACCATGGATCTTTTATCAATACAGGACC-3', 10 pmol of the primer 5'-GGCACCGGCGGTCATGATCCAATTCCTTTGTGTG-3', 20 ng DNA of pBSDXSBACSU plasmid, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 120 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the

mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis. The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.4 µg of the vector pACYC184 (Chang and Cohen 1978, NEB) and 1.8 µg of the purified PCR product are digested with *Nru*I and *Eag*I in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 19 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYCdxs. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYCdxs is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYCdxs is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (dbj D84432).

2.0 µg of the vector pACYCdxs and 8 µg of the vector pBScyclo (see example XXx) are digested with *Eag*I and *Sal*I in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the digested and purified pACYCdxs vector DNA and 30 ng of a by DNA electrophoresis separated and purified 2.7 kb *Eag*I/*Sal*I fragment (containing the ORFs *xy*I/B and *isp*C from *E. coli*) are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYCdxsxyIBispC. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYCdxsxyIBispC is isolated with the

plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYCdxsxyIBispC is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions.

Example 35

Construction of a vectors carrying the *dxs*, *xyIB*, *ispC*, and *ispG* and optionally *ispH* genes capable for the transcription and expression thereof

The *E. coli* ORF *ispH* (*lytB*) (accession no. gb AE000113) from base pair (bp) position 5618 to 6568 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-GCTTGCCTCGACGAGGAGAAATTAACCATGCAGATCCTGTTGCCACC-3', 10 pmol of the primer 5'-GCTGCTCTCGAGTTAATCGACTTCACGAATATCG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.5 µg of the vector pACYCdxsxyIBispC (see example 34) are linearized with *Sall* and 0.9 µg of the purified PCR product are digested with *Sall* and *XhoI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

15 ng of the purified vector DNA and 18 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pACYCdxsxyIBispClytB. The ligation mixture is incubated for 2 h at 25 °C.

1 μ l of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pACYCdxsxyIBispClytB is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pACYCdxsxyIBispClytB is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000113).

The *E. coli* ORF *ispG* (*gcpE*) (accession no. gb AE000338) from base pair (bp) position 372 to 1204 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5' - GGTCGAGTCGACGAGGAGAAATTAACCATGCATAACCAGGCTCCAATTC-3', 10 pmol of the primer 5'-CCCATCCTCGAGTTATTTTCAACCTGCTGAACGTC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 μ l containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 μ l is subjected to agarose gel electrophoresis. The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

Each 2.0 μ g of the vectors pACYCdxsxyIBispC (see example 34) and pACYCdxsxyIBispClytB (see above) are linearized with *SalI* and 1.1 μ g of the purified PCR product are digested with *SalI* and *XhoI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

18 ng of the purified vector DNAs and 23 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 μ l of T4-Ligase buffer (Gibco) in a total volume of 10 μ l, yielding the plasmids pACYCdxsxyIBispCgcpE and pACYCdxsxyIBispClytBgcpE. The ligation mixtures are incubated for 2 h at 25 °C. 1 μ l of the ligation mixture is transformed into

electrocompetent *E. coli* XL1-Blue cells. The plasmids pACYCdxsxyIBispCgcpE and pACYCdxsxyIBispClytBgcpE are isolated with the plasmid isolation kit from Qiagen.

The DNA inserts of the plasmids pACYCdxsxyIBispCgcpE and pACYCdxsxyIBispClytBgcpE are sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. They are identical with the DNA sequence of the database entry (gb AE000338).

Example 36

Incorporation experiment with recombinant *Escherichia coli* XL1-pACYCdxsxyIBispCgcpE using [U-¹³C₆]glucose

0.2 litre of Terrific Broth (TB) medium containing 5 mg of chloramphenicol are inoculated with *E. coli* strain XL1-Blue harbouring the plasmid pACYCdxsxyIBispCgcpE. The cells are grown in a shaking culture at 37 °C overnight. At an optical density (600 nm) of 1.7-2.4 a solution containing 1 g of lithium lactate (10 mmol), 200 mg [U-¹³C₆]glucose (1.1 mmol) at a final volume of 24 ml (pH=7.4) are added continuously within 2 hours. Then, after 1 hour an aliquot of 40 ml was taken and centrifuged for 20 min at 5,000 rpm and 4 °C. The cells are washed with water containing 0.9 % NaCl and centrifuged as described above. The cells are suspended in 700 µl of a mixture of methanol-d₄ and D₂O (6:4, v/v) containing 10 mM NaF, cooled on ice and sonified 3 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 90 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm for 15 min. NMR spectra of the cell free extracts are recorded directly with a Bruker AVANCE DRX 500 spectrometer (Karlsruhe, Germany). In order to avoid degradation during work-up, the structures of the products are determined by NMR spectroscopy without further purification.

The ¹³C-NMR spectra showed signals accounting for 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate (cf. Tables 2 and 4, example 18) as major product. A formation of 2C-methyl-D-erythritol 2,4-cyclodiphosphate could not be detected.

Example 37

Incorporation experiment with recombinant *Escherichia coli* XL1-pACYCdxsxyIBispClytBgcpE using glucose

Example 36 can be carried out with recombinant *Escherichia coli* XL1-pACYCdxsxyIBispClytBgcpE using glucose for converting glucose to isopentenyl diphosphate and/or dimethylallyl diphosphate.

Example 38

Cloning of the *ispG* gene of *Escherichia coli* and expression as maltose binding fusion protein (MBP-IspG)

The *E. coli* ORF *ispG* (*gcpE*) (accession no. gb AE000338) from base pair (bp) position 372 to 1204 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-GAACCGGAATTCATGCATAACCAGGCTCCAATTC-3', 10 pmol of the primer 5'-CGAGCGGATCCCATCACG-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 60 sec at 94 °C, 60 sec at 50 °C and 90 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.2 µg of the vector pMAL-C2 (NEB) and 0.8 µg of the purified PCR product are digested with *EcoRI* and *BamHI* in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR purification kit from Qiagen.

20 ng of the purified vector DNA and 15 ng of the purified PCR product are ligated together

with 1 U of T4-Ligase (Gibco), 2 µl of T4-Ligase buffer (Gibco) in a total volume of 10 µl, yielding the plasmid pMALgcpE. The ligation mixture is incubated for 2 h at 25 °C. 1 µl of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pMALgcpE is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pMALgcpE is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000338).

Example 39

Cloning of the *ispH* gene of *Escherichia coli* and expression as maltose binding fusion protein (MBP-IspH)

The *E. coli* ORF *ispH* (*lytB*) (accession no. gb AE000113) from base pair (bp) position 5618 to 6568 is amplified by PCR using chromosomal *E. coli* DNA as template. The reaction mixture contains 10 pmol of the primer 5'-TGGAGGGGATCCATGCAGATCCTGTGGCCACC-3', 10 pmol of the primer 5'-GCATTTCTGCAGAACTTAGGC-3', 20 ng of chromosomal DNA, 2 U of Taq DNA polymerase (Eurogentec) and 20 nmol of dNTPs in a total volume of 100 µl containing 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-hydrochloride, pH 8.8 and 0.1 % (w/w) Triton X-100.

The mixture is denaturated for 3 min at 94 °C. Then 30 PCR cycles for 45 sec at 94 °C, 45 sec at 50 °C and 60 sec at 72 °C followed. After further incubation for 10 min at 72 °C, the mixture is cooled to 4 °C. An aliquot of 2 µl is subjected to agarose gel electrophoresis.

The PCR amplificate is purified with the PCR purification kit from Qiagen (Hilden).

2.2 µg of the vector pMAL-C2 (NEB) and 0.7 µg of the purified PCR product are digested with *Bam*HI and *Pst*II in order to produce DNA fragments with overlapping ends. The restriction mixtures are prepared according to the conditions supplied by the customer (NEB) and are incubated for 3 h at 37 °C. Digested vector DNA and PCR product are purified using the PCR

purification kit from Qiagen.

20 ng of the purified vector DNA and 14 ng of the purified PCR product are ligated together with 1 U of T4-Ligase (Gibco), 2 μ l of T4-Ligase buffer (Gibco) in a total volume of 10 μ l, yielding the plasmid pMALytB. The ligation mixture is incubated for 2 h at 25 °C. 1 μ l of the ligation mixture is transformed into electrocompetent *E. coli* XL1-Blue cells. The plasmid pMALytB is isolated with the plasmid isolation kit from Qiagen.

The DNA insert of the plasmid pMALytB is sequenced by the automated dideoxynucleotide method using an ABI Prism 377™ DNA sequencer from Perkin Elmer with the ABI Prism™ Sequencing Analysis Software from Applied Biosystems Divisions. It is identical with the DNA sequence of the database entry (gb AE000113).

Example 40

Preparation and purification of recombinant IspG maltose binding fusion protein (MRP-IspG)

0.5 liter of Luria Bertani (LB) medium containing 90 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harboring plasmid pMALgcpE. The culture is grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.7, the culture is induced with 2 mM IPTG. The culture is grown for further 5 h. The cells are harvested by centrifugation for 20 min at 5,000 rpm and 4 °C. The cells are washed with 20 mM Tris hydrochloride pH 7.4, centrifuged as above and frozen at -20 °C for storage.

2 g of the cells are thawed in 20 ml of 20 mM Tris hydrochloride pH 7.4, 0.2 M sodium chloride and 0.02 % (g/v) sodium acetate (buffer A) in the presence of 1 mg ml⁻¹ lysozyme and 100 μ g ml⁻¹ DNaseI. The mixture is incubated at 37 °C for 30 min, cooled on ice and sonified 6 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 70 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm at 4 °C for 30 min. The cell free extract is applied on a column of amylose resin FF (column volume 25 ml, NEB) previously equilibrated with buffer A at a flowrate of 2 ml min⁻¹. The column is washed with 130 ml of buffer A. MRP-IspG is eluted with a linear gradient of 0-10 mM maltose in buffer A. MRP-IspG containing fractions are combined according to SDS-PAGE and dialyzed overnight against 100 mM Tris hydrochloride pH 7.4. The homogeneity of MRP-IspG is judged by SDS-

PAGE. One band at 84 kDa is visible, which is in line with the calculated molecular mass. The yield of pure MRP-IspG is 9 mg.

Example 41

Preparation and purification of recombinant IspH maltose binding fusion protein (MRP-IspH)

0.5 liter of Luria Bertani (LB) medium containing 90 mg of ampicillin are inoculated with 10 ml of an overnight culture of *E. coli* strain XL1-Blue harboring plasmid pMALyTB. The culture is grown in a shaking culture at 37 °C. At an optical density (600 nm) of 0.7, the culture is induced with 2 mM IPTG. The culture is grown for further 5 h. The cells are harvested by centrifugation for 20 min at 5,000 rpm and 4 °C. The cells are washed with 20 mM Tris hydrochloride pH 7.4, centrifuged as above and frozen at -20 °C for storage.

2 g of the cells are thawed in 20 ml of 20 mM Tris hydrochloride pH 7.4, 0.2 M sodium chloride and 0.02 % (g/v) sodium azide (buffer A) in the presence of 1 mg ml⁻¹ lysozyme and 100 µg ml⁻¹ DNaseI. The mixture is incubated at 37 °C for 30 min, cooled on ice and sonified 6 x 10 sec with a Branson Sonifier 250 (Branson SONIC Power Company) set to 70 % duty cycle output, control value of 4 output. The suspension is centrifuged at 15,000 rpm at 4 °C for 30 min. The cell free extract is applied on a column of amylose resin FF (column volume 25 ml, NEB) previously equilibrated with buffer A at a flowrate of 2 ml min⁻¹. The column is washed with 130 ml of buffer A. MRP-IspH is eluted with a linear gradient of 0-10 mM maltose in buffer A. MRP-IspH containing fractions are combined according to SDS-PAGE and dialyzed overnight against 100 mM Tris hydrochloride pH 7.4. The homogeneity of MRP-IspH is judged by SDS-PAGE. One band at 78 kDa is visible, which is in line with the calculated molecular mass. The yield of pure MRP-IspH is 14 mg.

Example 42

Synthesis of 1-hydroxy-2-methyl-but-2-enyl-4-diphosphate (see Fig. 7)

4-Chloro-2-methyl-2-buten-1-ol (Choi et al. (1999) J. Org. Chem. 64, 8051-8053)

A solution containing 1.17 ml of 2-methyl-2-vinyl-oxirane (12 mmol), 1.6 g of CuCl₂ (12 mmol) and 510 mg of LiCl (12 mmol) in 10 ml of ethylacetate was heated to 80 °C for 30 min. The

reaction was stopped by adding 50 g of ice. The mixture was filtered through a sintered glass funnel under reduced pressure. 100 ml of CH_2Cl_2 was added and the organic phase was separated. The aqueous layer was extracted two times with 100 ml of CH_2Cl_2 . The combined organic phase was dried over anhydrous MgSO_4 , filtered, and concentrated. The crude product was purified by chromatography over silica gel (CH_2Cl_2 , 3 x 37 cm) to yield 0.755 g of a yellow liquid (6.4 mmol, 53 %).

^1H NMR (CDCl_3 , 500 MHz) δ 9.43 (s, 1H), 6.50 (t, $J=7.5$ Hz, 1H), 4.24 (d, $J=7.5$ Hz, 2H), 1.77 (s, 3H)

^{13}C NMR (CDCl_3 , 125 MHz) δ 194.3, 145.7, 141.1, 38.6, 9.1

4-Chloro-2-methyl-2-buten-1-al-dimethyl-acetal

A solution of 184 mg 4-chloro-2-methyl-2-buten-1-al (1.55 mmol), 600 μl of $\text{HC}(\text{OMe})_3$ (5.6 mmol) and a catalytic amount of p-TsOH was incubated for 3 h at room temperature. The crude mixture was purified by chromatography over silica gel (n-hexane/ethylacetate 7:3) to yield 177 mg of a colourless liquid (1.08 mmol, 72 %).

^1H NMR (CDCl_3 , 500 MHz) δ 5.78 (t, 1H, $J=7.9$), 4.47 (s, 1H), 4.15 (d, $J=7.9$ Hz, 2H), 3.33 (s, 6 H), 1.73 (s, 3H)

^{13}C NMR (CDCl_3 , 125 MHz) δ 137.6, 124.4, 106.0, 53.5, 39.6, 11.4

(E)-3-Formyl-2-buten-1-diphosphate triammonium salt (Davisson et al. (1986) *J. Org. Chem.*, 51, 4768)

To a solution of 4-chloro-2-methyl-2-buten-1-al-dimethyl-acetal chloride (25 mg, 0.15 mmol) in 250 μl of MeCN a solution of 0.162 g (0.18 mmol) of tris(tetra-n-butylammonium) hydrogen pyrophosphate in 400 μL of MeCN was added slowly at room temperature, leading to an orange-red solution. After 2 h the reaction was finished and the solvent was removed under reduced pressure. The orange oil was dissolved in 3 mL of H_2O and passed through a column of DOWEX 50 WX8 (1 x 4 cm) cation-exchange resin (NH_4^+ form) that has been equilibrated with 20 mL of 25 mM NH_4HCO_3 . The column was eluted with 20 mL of 25 mM NH_4HCO_3 . The resulting solution was lyophilized. The obtained solid was dissolved in 2 ml water and acidified with aqueous HCl to pH=3. After 2 minutes the solution was neutralized and lyophilized.

^1H NMR (D_2O , 360 MHz) δ 9.37 (s, 1H), 6.86 (t, 1H, 5.6Hz), 4.85 (dd, $J=7.9$, $J=5.8$ Hz, 2H), 1.72 (s, 3H)

^{13}C NMR (D_2O , 90 MHz) δ 199.2, 153.1 (d, $J=7.5$ Hz), 138.5, 63.2 (d, $J=4.9$), 8.5

[1-³H]1-hydroxy-2-methyl-but-2-enyl-4-diphosphate

A solution containing 50 mCi (15 μ mol) NaBH₃T, 15 μ mol 3-formyl-2-buten-1-diphosphate triammonium salt and 100 mM Tris/HCl pH=8 was incubated for 30 minutes at room temperature. The solution was acidified by adding 1 M HCl to pH=2. After 2 minutes the solution was neutralized by adding 1 M NaOH.

The product was characterized by ion-exchange chromatography (see examples 20 and 25).

Example 43 **$\gamma\delta$ T cell stimulation assays**

PBMCs from healthy donors (donor A and donor B) are isolated from heparinized peripheral blood by density centrifugation over Ficoll-Hypaque (Amersham Pharmacia Biotech, Freiburg, Germany). 5×10^5 PBMCs/well are cultivated in 1 mL RPMI 1640 medium supplemented with 10% human AB serum (Klinik rechts der Isar, München, Germany), 2 mM L-glutamine, 10 μ M mercaptoethanol. Amounts of recombinant human IL-2 (kindly provided by Eurocetus, Amsterdam, The Netherlands) and substrates are varied from 1 to 10 U and 10 to 0.1 μ M, respectively. 20 μ M IPP (Echelon, Research Laboratories Inc., Salt Lake City, USA) serves as a positive control whereas medium alone serves as negative control. Incubation is done for seven days at 37 °C in the presence of 7% CO₂. The harvested cells are double-stained with fluorescein isothiocyanate (FITC)-conjugated mouse anti-human monoclonal antibody V δ 2 TCR and phycoerythrin (PE)-conjugated monoclonal CD3 antibody. The cells are analyzed using a FACScan supported with Cellquest (Becton Dickinson, Heidelberg, Germany).

The substrates (E)-1-hydroxy-3-methyl-but-2-enyl 4-diphosphate (HMBPP) and 3-formyl-but-2-enyl 1-diphosphate (Aldehyd) were prepared synthetically as described above.

It is found that both synthetically prepared substrates (HMBPP and Aldehyd) show at least double stimulation compared to IPP when used at a concentration that is 200-fold lower than the concentration of the IPP sample (Table 8).

Table 8. Activation of $\gamma\delta$ T-cells by phosphororganic compounds

Substrate	Concentration [μ M]	IL-2 [U]	% $\gamma\delta$ T-cells	
			Donor A	Donor B
Medium	-	1	1.51	2.75
Medium	-	5	1.45	2.23
Medium	-	10	1.32	1.68
IPP	20	1	8.19	6.24
IPP	20	5	14.42	9.32
IPP	20	10	16.6	11.86
IPP	1	1	1.56	2.22
IPP	1	5	1.59	2.67
IPP	1	10	1.71	2.19
IPP	0.1	1	1.3	2.15
IPP	0.1	5	1.3	2.26
IPP	0.1	10	1.01	2.54
HMBPP	10	1	3.3	31.42
HMBPP	10	5	17.38	63.48
HMBPP	10	10	24.94	63.34
HMBPP	1	1	5.57	35.34
HMBPP	1	5	14.4	54.12
HMBPP	1	10	19.85	55.90
HMBPP	0.1	1	11.78	32.21
HMBPP	0.1	5	22.92	44.69
HMBPP	0.1	10	34.69	36.33
HMBPP/IPP	0.5/0.5	1	7	30.35
HMBPP/IPP	0.5/0.5	5	15.38	53.76
HMBPP/IPP	0.5/0.5	10	24.19	46.58
Aldehyd	10	1	12.19	30.69
Aldehyd	10	5	34.69	30.33
Aldehyd	10	10	38.99	38.85
Aldehyd	1	1	15.91	21.18
Aldehyd	1	5	40.13	30.76
Aldehyd	1	10	48.28	36.69
Aldehyd	0.1	1	10	13.54
Aldehyd	0.1	5	19.77	18.45
Aldehyd	0.1	10	21.93	25.82
Aldehyd/IPP	0.5/0.5	1	13.98	22.11
Aldehyd/IPP	0.5/0.5	5	33.94	32.06
Aldehyd/IPP	0.5/0.5	10	42.84	36.25

IPP: isopentenyl diphosphate

HMBPP: (E)-1-hydroxy-3-methyl-but-2-enyl 4-diphosphate

Aldehyd: (E)-3-formyl-but-2-enyl 1-diphosphate (prepared according to example 42)

Example 44

High through-put screening assay of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate

synthase (IspG) activity

Assay mixtures contain 20 mM potassium phosphate, pH 7.0, 0.4 mM NADH, 0.5 mM CoCl_2 , 0.2 mM 2C-methyl-D-erythritol 2,4-cyclodiphosphate, and 50 μl protein in a total volume of 1 ml. The mixtures are incubated at 37 °C. The oxidation of NADH is monitored photometrically at 340 nm. Alternatively, the concentration of NADH is determined by measuring the relative fluorescence of NADH at 340 nm excitation/460 nm emission.

Example 45

High through-put screening assay of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (IspH) activity

Assay mixtures contain 20 mM potassium phosphate, pH 7.0, pH 8.0, 0.4 mM NADH, 20 μM FAD, 0.5 mM CoCl_2 , 0.2 mM 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate, and 50 μl protein in a total volume of 1 ml. The mixtures are incubated at 37 °C. The oxidation of NADH is monitored photometrically at 340 nm. Alternatively, the concentration of NADH is determined by measuring the relative fluorescence of NADH at 340 nm excitation/460 nm emission.

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Claims

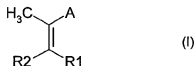
1. A protein in a form that is functional for the enzymatic conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate notably in its (*E*)-form.
2. The protein according to claim 1, wherein it is functional for said conversion in the presence of NADH and/or NADPH.
3. The protein according to claim 2, wherein it is functional for said conversion in the presence of Co^{2+} .
4. The protein according to one of claims 1 to 3, wherein it has a sequence encoded by the *ispG* (formerly *gcpE*) gene of *E. coli* or a function-conservative homologue of said sequence.
5. A protein in a form that is functional for the enzymatic conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its (*E*)-form, to isopentenyl diphosphate and/or dimethylallyl diphosphate.
6. The protein according to claim 5, wherein it is in a form functional for said conversion in the presence of FAD and NAD(P)H.
7. The protein according to claim 6, wherein it is in a form functional for said conversion in the presence of a metal ion selected from the group of manganese, iron, cobalt, or nickel ion.
8. The protein according to one of claims 5 to 7, wherein it has a sequence encoded by the *ispH* (formerly *lytB*) gene of *E. coli* or a function-conservative homologue of said sequence.
9. The protein according to one of claims 1 to 8, wherein it is a plant protein, notably from *Arabidopsis thaliana*.

10. The protein according to one of claims 1 to 8, wherein it is a bacterial protein, notably from *E. coli*.
11. The protein according to one of claims 1 to 8, wherein it is a protozoal protein, notably from *Plasmodium falciparum*.
12. Purified isolated nucleic acid encoding the protein according to one of claims 1 to 4 and/or the protein according to one of claim 5 to 8 with or without introns.
13. A DNA expression vector containing the sequence of the nucleic acid according to claim 12.
14. Use of a protein according to one of claims 1 to 11 for screening a chemical library for an inhibitor of the biosynthesis of isoprenoids.
15. Cells, cell cultures, organisms or parts thereof recombinantly endowed with the sequence of the nucleic acid according to claim 12 or with the vector according to claim 13, wherein said cell is selected from the group consisting of bacterial, protozoal, fungal, plant, insect and mammalian cells.
16. Cells, cell cultures, organisms or parts thereof according to claim 15, wherein it is recombinantly endowed with a vector containing a nucleic acid sequence encoding a protein according to one of claims 1 to 4 and/or a protein according to one of claims 5 to 8, and wherein said cell is optionally further endowed with at least one gene selected from the following group: *dxs*, *dxr*, *ispD* (formerly *ygbP*); *ispE* (formerly *ygbB*); *ispF* (formerly *ygbB*) of *E. coli* or a function-conservative homologue thereof, or a function-conservative fusion, deletion or insertion variant of any of the above genes.
17. Cells, cell cultures, or organisms or parts thereof transformed or transfected for an increased rate of formation of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably in its (*E*)-form, compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection.

18. Cells, cell cultures, or organisms or parts thereof transformed or transfected for an increased rate of conversion of (E)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate to isopentenyl diphosphate and/or dimethylallyl diphosphate compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection.
19. Cells, cell cultures, or organisms or parts thereof according to claim 15 transformed or transfected for an increased expression level of the protein of one of claims 1 to 4 and/or the protein of one of claims 5 to 8 compared to cells, cell cultures, or organisms or parts thereof absent said transformation or transfection.
20. Cells, cell cultures or organisms or parts thereof in accordance with claim 15 or 16, characterized by the recombinant endowment with sets of genes as follows:
ispC (formerly *dxr*), *ispD*, *ispE*, *ispF*, *ispG* (formerly *gcpE*); or
ispC, *ispD*, *ispE*, *ispF*, *ispG*, *ispH* (formerly *lytB*); or
dxs, *ispC*, *ispD*, *ispE*, *ispF*, *ispG*; or
dxs, *ispC*, *ispD*, *ispE*, *ispF*, *ispG*, *ispH*; or
dxs, *ispC*, *ispG*; or
dxs, *ispC*, *ispG*, *ispH*
of *E. coli* or a function-conservative homologue thereof and/or a function-conservative fusion, deletion or insertion variant of any of the above genes.
21. Cells, cell cultures or organisms or parts thereof in accordance with claim 20, characterized by further recombinant endowment(s) with gene(s) being functional for biosynthetic steps downstream from the C5 isoprenoids.
22. Cells, cell cultures or organisms or parts thereof in accordance with one of claims 15 to 21, wherein at least one gene of said recombinant endowments is equipped with artificial ribosomal binding site(s) for expression of the corresponding gene product(s) at a rate enhanced compared to the rate in the absence of the artificial ribosomal binding site(s).
23. Cells, cell cultures or organisms or parts thereof in accordance with one of claims 15 to 22, wherein at least one of said recombinant endowments is due to a high copy replication vector.

24. Cells, cell cultures or organisms or parts thereof in accordance with one of claims 15 to 23, wherein they are of bacterial, protozoal, fungal, plant or animal origin.
25. Use of the cells, cell cultures or organisms, or parts thereof in accordance with one of claims 15 to 24 or disruption products thereof for the enhanced rate of *in vivo* formation or for the efficient *in vitro* production of an, optionally isotopically labelled, biosynthetic intermediate or product of the non-mevalonate isoprenoid biosynthetic pathway, optionally by feeding 1-deoxy-D-xylulose or glucose that may be isotopically labelled.
26. Use according to claim 25, wherein said intermediate or product is a C5-isoprenoid intermediate compound; or a >C5-isoprenoid compound; or a terpenoid compound.
27. Use according to one of claims 25 or 26, wherein the rate of formation or production is enhanced by providing a source for CTP.
28. Use according to claim 27, wherein the source for CTP is cytidine and/or uridine and/or cytosine and/or uracil and/or ribose and and/or ribose 5-phosphate and/or any biosynthetic precursor of CTP.
29. Use according to one of claims 25 to 28, wherein the rate of formation or production is enhanced by providing a source for phosphorylation enhancement.
30. Use according to claim 29, wherein the source for phosphorylation enhancement is glycerol 3-phosphate and/or phosphoenolpyruvate and/or inorganic phosphate and/or inorganic pyrophosphate and/or any organic phosphate or pyrophosphate.
31. Use according to one of claims 25 to 30, wherein the rate of formation or production is enhanced by providing a source for reduction equivalents.
32. Use according to claim 31, wherein the source for reduction equivalents is succinate and/or lipids and/or glucose and/or glycerol and/or lactate.

33. Optionally isotope-labelled compound of the following formula I or a salt thereof:



whereby R^1 and R^2 are different from each other and one of R^1 and R^2 is hydrogen and the other is selected from the group consisting of $-\text{CH}_2\text{-O-PO(OH)-O-PO(OH)}_2$, $-\text{CH}_2\text{-O-PO(OH)}_2$, and $-\text{CH}_2\text{OH}$, and whereby A stands for $-\text{CH}_2\text{OH}$ or $-\text{CHO}$.

34. The optionally isotope-labelled compound according to claim 33, wherein A stands for $-\text{CH}_2\text{OH}$.
35. The optionally isotope-labelled compound according to claim 33, wherein A stands for $-\text{CHO}$.
36. The optionally isotope-labelled compound according to one of claims 33 to 35, wherein R^1 is H and R^2 is selected from the group consisting of $-\text{CH}_2\text{-O-PO(OH)-O-PO(OH)}_2$ and $-\text{CH}_2\text{-O-PO(OH)}_2$.
37. The optionally isotope-labelled compound according to one of claims 33 to 35, wherein R^2 is H and R^1 is selected from the group consisting of $-\text{CH}_2\text{-O-PO(OH)-O-PO(OH)}_2$ and $-\text{CH}_2\text{-O-PO(OH)}_2$.
38. The optionally isotope-labelled compound according to one of claims 33 to 37, whereby said group consists of $-\text{CH}_2\text{-O-PO(OH)-O-PO(OH)}_2$.
39. Optionally isotope-labelled 1-hydroxy-2-methyl-2-butenyl 4-diphosphate salt or a protonated form thereof.
40. Optionally isotope-labelled (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate salt or a protonated form thereof.

41. Optionally isotope-labelled (Z)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate salt or a protonated form thereof.
42. Use of a compound according to one of claims 33 to 41, notably according to claim 38, for screening for genes, enzymes or inhibitors of the biosynthesis of isoprenoids or terpenoids, either *in vitro* in the presence of an electron donor or *in vivo*.
43. Use of a compound according to one of claims 33 to 41, notably according to claim 40, as an immunomodulatory agent.
44. Use of a compound according to one of claims 33 to 41, notably according to claim 40, for activating $\gamma\delta$ T cells.
45. Use of a compound according to one of claims 33 to 41, notably according to claim 40, for the preparation of a medicament.
46. Pharmaceutical composition containing a compound according to one of claims 33 to 41, notably according to claim 36 or 40, and a pharmaceutically acceptable carrier.
47. The pharmaceutical composition according to claim 46 further comprising an antibiotically active compound.
48. The pharmaceutical composition according to claim 47, wherein the antibiotically active compound is bacteriostatic.
49. The pharmaceutical composition according to claim 47, wherein the antibiotically active compound inhibits bacterial protein synthesis.
50. A method of treating a pathogen infection comprising administering a pharmaceutical composition according to one of claims 46 to 49.
51. Monoclonal or polyclonal antibody against a compound of one of claims 33 to 41.

52. A method of detecting a pathogen, notably in a body fluid, by using the antibody of claim 51.
53. Use of the cells, cell cultures or organisms or parts thereof in accordance with claims 15 to 24 for the production of a protein in an enzymatically competent form for the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate into 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate.
54. Use of the cells, cell cultures or organisms or parts thereof in accordance with claims 15 to 24 for the production of a protein in an enzymatically competent form for the conversion of (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate into isopentenyl diphosphate and/or dimethylallyl diphosphate.
55. Use of the cells, cell cultures or organisms or parts thereof in accordance with claims 15 to 24 for the production of proteins in an enzymatically competent form for the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate into isopentenyl diphosphate and/or dimethylallyl diphosphate.
56. A method of altering the expression level of the gene product(s) of *ispG* and/or *ispH* in cells comprising
- (a) transforming host cells with the *ispG* and/or *ispH* gene,
 - (b) growing the transformed host cells of step (a) under conditions that are suitable for the efficient expression of *ispG* and/or *ispH*, resulting in production of altered levels of the *ispG* and/or *ispH* gene product(s) in the transformed cells relative to expression levels of untransformed cells.
57. Method of identifying an inhibitor of an enzyme functional for the conversion of 2C-methyl-D-erythritol 2,4-cyclodiphosphate to 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably its *E*-form, of the non-mevalonate isoprenoid pathway by the following steps:
- (a) incubating a mixture containing said enzyme with its, optionally isotope-labeled, substrate 2C-methyl-D-erythritol-2,4-cyclodiphosphate under conditions suitable for said conversion in the presence and in the absence of a potential inhibitor,

- (b) subsequently determining the concentration of 2C-methyl-D-erythritol 2,4-cyclodiphosphate and/or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, and
 - (c) comparing the concentration in the presence and in the absence of said potential inhibitor.
58. Method of identifying an inhibitor of an enzyme functional for the conversion of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably its E-form, to isopentenyl diphosphate or dimethylallyl diphosphate of the non-mevalonate isoprenoid pathway by the following steps:
- (a) incubating a mixture containing said enzyme with its, optionally isotope-labeled, substrate 1-hydroxy-2-methyl-2-butenyl 4-diphosphate under conditions suitable for said conversion in the presence and in the absence of a potential inhibitor,
 - (b) determining the concentration of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate or dimethylallyl diphosphate, and
 - (c) comparing the concentration in the presence and in the absence of said potential inhibitor.
59. The method according to claim 58, wherein step (a) is carried out in the presence of FAD.
60. The method of one of claims 57 to 59, which further comprises preparing cells recombinantly endowed with a gene coding for said enzyme, culturing said cells, preparing a crude extract of said cells, and using said crude extract in step (a).
61. The method according to one of claims 57 to 60, wherein said enzyme is a plant enzyme.
62. The method according to one of claims 57 to 60, wherein said enzyme is an enzyme of *Plasmodium falciparum*.
63. The method according to one of claims 57 to 60, wherein said enzyme is a bacterial enzyme.

64. The method according to one of claims 57 to 60, wherein the incubation of step (a) is carried out in the presence of a sulfhydryl reductant e.g. dithiothreitol.
65. The method according to one of claims 57 to 64, wherein the incubation in step (a) is carried out in the presence of a phosphatase inhibitor.
66. The method according to claim 65, wherein the phosphatase inhibitor is an alkali fluoride.
67. The method according to one of claims 57 to 66, wherein the incubation of step (a) is carried out in the presence of NADH or NADPH.
68. The method according to one of claims 57 to 67, wherein the incubation in step (a) is carried out in the presence of an inhibitor of an enzyme acting downstream of isopentenyl diphosphate or dimethylallyl diphosphate.
69. The method according to one of claims 57 to 68, wherein the incubation of step (a) is carried out in the presence of a salt selected from the group of Co^{2+} , Mn^{2+} , Fe^{2+} , Ni^{2+} salts.
70. The method according to one of claims 57 to 69, wherein step (b) is carried out by reversed phase ion-pair HPLC chromatography.
71. The method according to one of claims 57 to 69, wherein step (b) is carried out by determining the consumption of NADH or NADPH.
72. The method according to one of claims 57 to 71, which is carried out on many potential inhibitors simultaneously or consecutively in a high-throughput screening.
73. A process for the efficient *in vivo* synthesis of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate; or isopentenyl

diphosphate or dimethylallyl diphosphate; optionally isotope labelled, in salt form or in protonated form, by the following steps:

- (a) culturing cells, preferably bacterial cells, recombinantly endowed in accordance with one of claims 15 to 24 for said synthesis for a predetermined period of time at a predetermined temperature;
- (b) optionally adding glucose to a predetermined final concentration and further culturing for a predetermined period of time;
- (c) harvesting the cells;
- (d) preparing a crude extract from the harvested cells;
- (e) separating and purifying optionally isotope-labelled 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate; or isopentenyl diphosphate; or dimethylallyl diphosphate; in salt form or in protonated form, optionally by preparative chromatography.

74. A process for screening chemical libraries for the presence or absence of inhibition of the biosynthesis of isoprenoids, notably by blocking the biosynthesis of the intermediates 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate and/or dimethylallyl diphosphate, said screening comprising:

- (a) culturing cells, preferably bacterial cells, recombinantly endowed in accordance with claim 15 for a predetermined period of time at a predetermined temperature;
- (b) optionally adding glucose to a predetermined final concentration and further culturing for a predetermined period of time;
- (c) harvesting the cells;
- (d) preparing a crude extract from the harvested cells;

whereby steps (a) to (d) are carried out in the presence and in the absence of a prospective inhibitor;

- (e) detecting difference(s) in the level(s) of 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate and/or dimethylallyl diphosphate; between the presence and absence of the prospective inhibitor; and

- (f) correlating said detected difference(s) with the presence or absence of an above-defined inhibition.
75. Cells, cell cultures or organisms or parts thereof for the efficient formation of a biosynthetic product or intermediate of the non-mevalonate pathway to isoprenoids or terpenoids, characterized by
- (a) first recombinant endowment with a gene functional for the biosynthesis of 1-deoxy-D-xylulose 5-phosphate from 1-deoxy-D-xylulose;
 - (b) capability for the uptake of 1-deoxy-D-xylulose; and
 - (c) recombinant endowment(s) with gene(s) being functional for the conversion of 1-deoxy-D-xylulose 5-phosphate into desired downstream C5-intermediate(s) of said pathway.
76. Cells, cell cultures or organisms or parts thereof in accordance with claim 75, wherein said gene(s) of said second recombinant endowment(s) code(s) for enzyme(s) for the formation of at least one of the following C5-intermediates of the non-mevalonate isoprenoid pathway:
- (a) 2C-methyl-D-erythritol 4-phosphate;
 - (b) 4-diphosphocytidyl-2C-methyl-D-erythritol;
 - (c) 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate;
 - (d) 2C-methyl-D-erythritol 2,4-cyclodiphosphate;
 - (e) 1-hydroxy-2-methyl-2-butenyl 4-diphosphate;
 - (f) isopentenyl diphosphate;
 - (g) dimethylallyl diphosphate.
77. Cells, cell cultures or organisms or parts thereof in accordance with claim 75 or 76, characterized by the recombinant endowment with sets of genes as follows:
- (a) *xyiB*, *dxr*, or
 - (b) *xyiB*, *dxr*, *ispD* (formerly *ygbP*); or
 - (c) *xyiB*, *dxr*, *ispD*, *ispE* (formerly *ychB*); or
 - (d) *xyiB*, *dxr*, *ispD*, *ispE*, *ispF* (formerly *ygbB*); or
 - (e) *xyiB*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG* (formerly *gcpE*); or
 - (f) *xyiB*, *dxr*, *ispD*, *ispE*, *ispF*, *ispG*, *ispH* (formerly *lytB*)

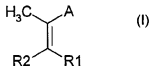
of *E. coli* or a function-conservative homologue thereof and/or a function-conservative fusion, deletion or insertion variant of any of the above genes.

78. Cells, cell cultures or organisms or parts thereof in accordance with claim 75, characterized by the recombinant endowment with *xylB* and *ispG* (formerly *gcpE*) and optionally at least one gene selected from the following group: *dxr*; *ispD* (formerly *ygbP*); *ispE* (formerly *ychB*); *ispF* (formerly *ygbB*) of *E. coli* or a function-conservative homologue thereof, or a function-conservative fusion, deletion or insertion variant of any of the above genes.
79. Cells, cell cultures or organisms or parts thereof in accordance with claim 75, characterized by the recombinant endowment with *xylB* and *ispH* (formerly *lytB*) and optionally at least one gene selected from the following group: *dxr*; *ispD* (formerly *ygbP*); *ispE* (formerly *ychB*); *ispF* (formerly *ygbB*); *ispG* (formerly *gcpE*) of *E. coli* or a function-conservative homologue thereof, or a function-conservative fusion, deletion or insertion variant of any of the above genes.
80. Cells, cell cultures or organisms or parts thereof in accordance with claim 75, characterized by the recombinant endowment with *xyl*, *ispG*, (formerly *gcpE*) and *ispH* (formerly *lytB*) and optionally at least one gene selected from the following group: *dxr*; *ispD* (formerly *ygbP*); *ispE* (formerly *ychB*); *ispF* (formerly *ygbB*); of *E. coli* or a function-conservative homologue thereof, or a function-conservative fusion, deletion or insertion variant of any of the above genes.
81. A process for the efficient *in vivo* synthesis of 2C-methyl-D-erythritol 4-phosphate; or 4-diphosphocytidyl-2C-methyl-D-erythritol; or 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate; or 2C-methyl-D-erythritol 2,4-cyclodiphosphate; or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate; or isopentenyl diphosphate or dimethylallyl diphosphate; optionally isotope labelled, in salt form or in protonated form, by the following steps:
- (a) culturing cells, preferably bacterial cells, recombinantly endowed in accordance with one of claims 75 to 80 for said synthesis for a predetermined period of time at a predetermined temperature;

- (b) adding 1-deoxy-D-xylulose to a predetermined final concentration and further culturing for a predetermined period of time;
 - (c) harvesting the cells;
 - (d) preparing a crude extract from the harvested cells;
 - (e) separating and purifying optionally isotope-labelled 2C-methyl-D-erythritol 4-phosphate; or 4-diphosphocytidyl-2C-methyl-D-erythritol; or 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate; or 2C-methyl-D-erythritol 2,4-cyclodiphosphate; or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate; or isopentenyl diphosphate; or dimethylallyl diphosphate; in salt form or in protonated form, by preparative chromatography.
82. The process according to one of claims 73, 74 or 81, wherein step (a) is carried out in terrific broth medium.
83. The process according to one of claims 73, 74, 81 or 82, wherein a source for CTP, preferably cytidine or uridine, is added in step (a).
84. The process according to one of claims 73, 74 or 81 to 83, wherein a source of phosphorylation activity, preferably glycerol 3-phosphate and/or inorganic phosphate, is added in step (a).
85. The process according to one of claims 73, 74 or 81 to 84 wherein a source of reduction equivalents, preferably succinate and/or lipids and/or glucose and/or glycerol and/or lactate is added in step (a).
86. A process for screening chemical libraries for the presence or absence of inhibition of the biosynthesis of isoprenoids, notably by blocking the biosynthesis of the intermediates 2C-methyl-D-erythritol 4-phosphate and/or 4-diphosphocytidyl-2C-methyl-D-erythritol and/or 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate and/or 2C-methyl-D-erythritol 2,4-cyclodiphosphate and/or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (*E*)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate and/or dimethylallyl diphosphate, said screening comprising: (i) carrying out the steps (a) to (d) of claim 81, preferably in combination

with one of claims 82 to 85, in the presence and absence of a prospective inhibitor;
 (ii) detecting difference(s) in the level(s) of 1-deoxy-D-xylulose and/or 1-deoxy-D-xylulose 5-phosphate and/or 2C-methyl-D-erythritol 4-phosphate and/or 4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate and/or 2C-methyl-D-erythritol 2,4-cyclodiphosphate and/or 1-hydroxy-2-methyl-2-butenyl 4-diphosphate, notably (E)-1-hydroxy-2-methyl-2-butenyl 4-diphosphate and/or isopentenyl diphosphate and/or dimethylallyl diphosphate; between the presence and absence of a prospective inhibitor and (iii) correlating said detected difference(s) with the presence or absence of an above-defined inhibition.

87. The process according to claim 74 or 86, wherein said detecting of step (ii) is done by HPLC and/or NMR spectroscopy.
88. Vektor comprising a sequence coding for one of the recombinant endowments as defined in one of claims 75 to 80.
89. A process for the chemical preparation of a compound of formula I or a salt thereof:



wherein A represents $-\text{CH}_2\text{OH}$ and R^1 and R^2 are different from each other and one of R^1 and R^2 is hydrogen and the other is $-\text{CH}_2\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$, $-\text{CH}_2\text{O}-\text{PO}(\text{OH})_2$ or $-\text{CH}_2\text{OH}$ by the following steps:

- (a) converting a compound of the following formula (II):



wherein B is a protective group into a compound of the following formula (III) or (IV):

93



(III)



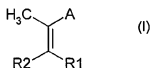
(IV)

by a Wittig or Horner reagent, wherein the group D is a precursor group convertible reductively to a $-\text{CH}_2\text{-OH}$ group;

- (b) reductively converting group D to a $-\text{CH}_2\text{-OH}$ group;
- (c) optionally converting group $-\text{CH}_2\text{-OH}$ obtained in step (b) into $-\text{CH}_2\text{-O-PO(OH)-O-PO(OH)}_2$ or $-\text{CH}_2\text{-O-PO(OH)}_2$ or salts thereof in a manner known per se;
- (d) optionally conversion to a desired salt;
- (e) removing the protective group B.

- 90. The process according to claim 89, wherein said protective group B forms an acetal together with the remaining moiety of the compound of formula (II).
- 91. The process according to claim 89 or 90, wherein said protective group B is a 2-tetrahydropyranyl group.
- 92. The process according to one of claims 89 to 91, wherein group D is an alkoxycarbonyl group.
- 93. The process according to one of claims 89 to 92, wherein said reduction of step (b) is performed with a metal hydride, notably an aluminium hydride or a boron hydride.
- 94. The process according to one of claims 89 to 93, wherein step (c) comprises converting said $-\text{CH}_2\text{-OH}$ group to a $-\text{CH}_2\text{-halide}$ group.
- 95. The process according to one of claims 89 to 94, wherein step (c) comprises reacting said $-\text{CH}_2\text{-OH}$ group with a sulfonic acid halogenide, notably tosyl chloride.
- 96. The process of one of claims 89 to 95, wherein step (c) comprises a reaction with phosphoric acid or diphosphoric acid or a salt thereof.

97. The process of one of claims 89 to 96, wherein steps (a) to (c) are carried out in aprotic solvents.
98. The process of one of claims 89 to 97, wherein step (e) is carried out by acid hydrolysis.
99. A process for the chemical preparation of a compound of formula I or a salt thereof:



wherein A represents $-\text{CH}_2\text{OH}$ or $-\text{CHO}$, R^1 is hydrogen, and R^2 is $-\text{CH}_2\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$, $-\text{CH}_2\text{O}-\text{PO}(\text{OH})_2$ or $-\text{CH}_2-\text{OH}$ by the following steps:

- (a) converting 2-methyl-2-vinyl-oxiran into 4-chloro-2-methyl-2-buten-1-al;
 - (b) converting 4-chloro-2-methyl-2-buten-1-al to its acetal;
 - (c) substituting the chlorine atom in the product of step (b) by a hydroxyl group, a phosphate group or a pyrophosphate group;
 - (d) hydrolysing the acetal obtained in step (c) to produce an aldehyde group;
 - (e) optionally converting the aldehyde group of the product of step (d) to a $-\text{CH}_2\text{OH}$ group.
100. The process of claim 99, wherein step (a) is carried out in the presence of CuCl_2 .
101. The process of claim 99 or 100, wherein step (b) is carried out in the presence of an ortho alkyl ester of formic acid.
102. The process of one of claims 99 to 101, wherein R^2 is $-\text{CH}_2\text{O}-\text{PO}(\text{OH})-\text{O}-\text{PO}(\text{OH})_2$ or $-\text{CH}_2\text{O}-\text{PO}(\text{OH})_2$ and step (c) is carried out by reacting the product of step (b) with a tetra-alkylammonium pyrophosphate or a tetra-alkylammonium phosphate, respectively, in a polar aprotic solvent.
103. The process of one of claims 99 to 102, wherein step (e) is performed with an alkali metal borohydride in aqueous solution.

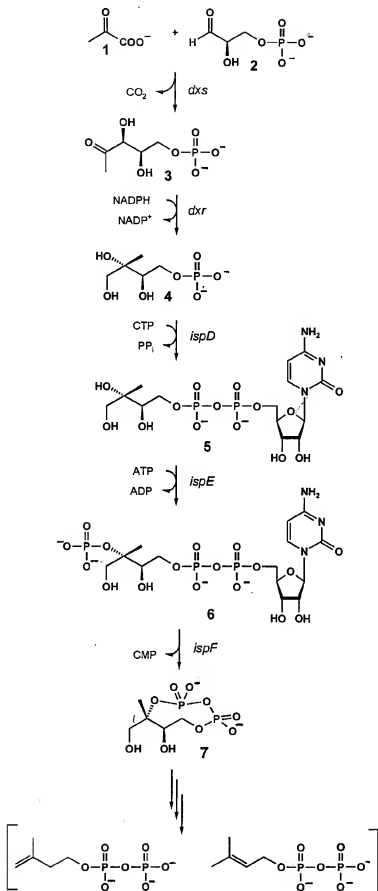


Fig. 1

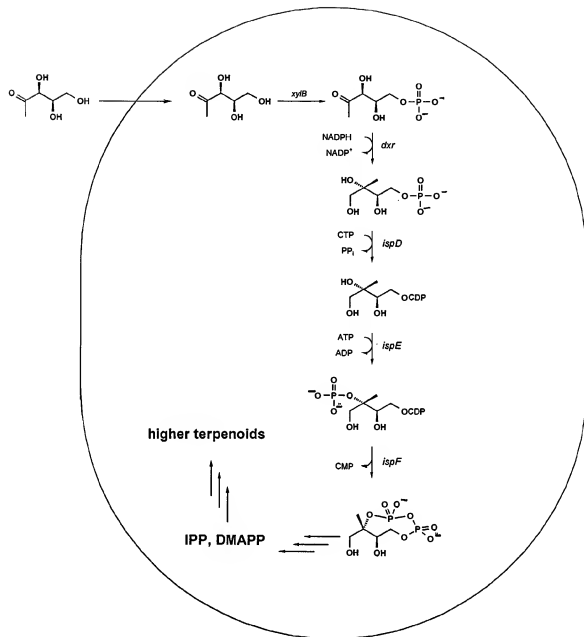


Fig. 2

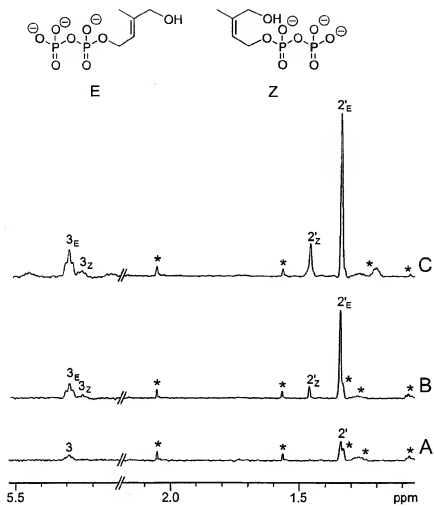


Fig. 3

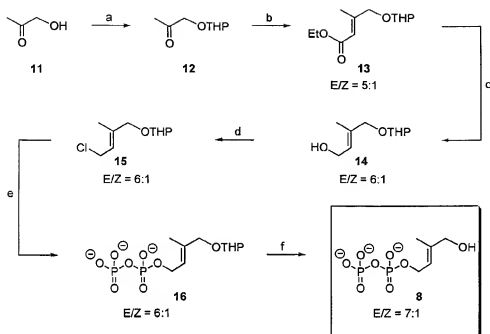


Fig. 4

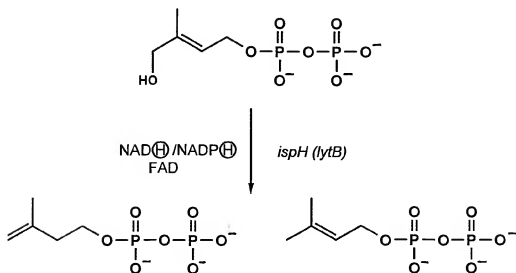


Fig. 5

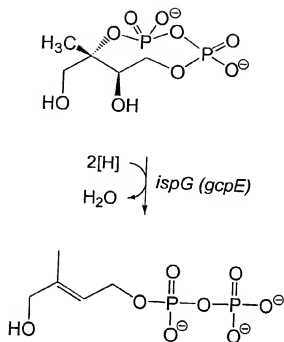


Fig. 6

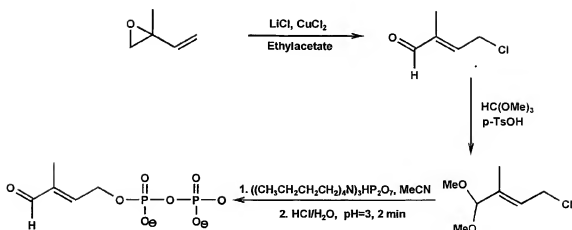


Fig. 7

Annex A

DNA sequence of the vector construct pBSxylBdxr

ID	PBSXYLBDXR	PRELIMINARY;	DNA;	5628 BP.
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SQ	SEQUENCE	5628 BP;	1378 A;	1374 C;	1552 G;	1324 T;	0 OTHER;
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Annex B

DNA sequence of the vector construct pBSxylBdxrispD

ID	PBSXYLBDXRISPD	PRELIMINARY;	DNA;	6354 BP.
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SQ	SEQUENCE	6354 BP;	1539 A;	1573 C;	1753 G;	1489 T;
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TGCGCGTAAC CACCACACCC GCCGCGCTTA ATGCGCGCT ACAGGGCGCG TCAG

Annex C

DNA sequence of the vector construct pBScyelo

ID PBSCYCLO PRELIMINARY; DNA; 7691 BP.

SQ SEQUENCE 7691 BP; 1844 A; 1888 C; 2148 G; 1811 T;

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TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATT AGAGCTTGAC GGGGAAAGCC
GGCGAACGTG GCGAGAAAAG AAGGGAAGAA AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC
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GGCGCGCTCA G

Annex D

DNA sequence of the vector construct pACYCgcpE

ID	PACYCGCPE	PRELIMINARY;	DNA;	5109 BP.
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SEQ	SEQUENCE	5109 BP;	1194 A;	1365 C;	1324 G;	1226 T;	0 OTHER;
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TGCCATACG

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Annex E

DNA sequence of the plasmid pBScaro14

ID	PBSCARO14	PRELIMINARY;	DNA;	7494 BP.SQ	SEQUENCE	7494 BP;
1722 A;	1935 C;	2026 G;	1811 T;			
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GGAAGAGTAT	GAGTATTCAA	CATTTCCGTG	TCGCGCTTAT	TCCTTTTTTT	CGGCGCATTT	
GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	AAAAGATGCT	GAAAGATCAGT	
TGGGTGCACG	AGTGGGTTAC	ATCGAACTGG	ATCTCAACAG	CGGTAAAGATC	CTTGAGAGTT	
TTGCGCCCGA	AGAAGCTTTT	CCAATGATGA	GCACCTTTTAA	AGTTCTGCTA	TGTGGCGCGG	
TATTATCCCG	TATTGACGCC	GGGCAAGAGC	AACCTCGGTCG	CCGCATACAC	TATTCTCAGA	
ATGACTTGGT	TGAGTACTCA	CCAGTCACAG	AAAJGATCTT	TACGGATGGC	ATGACAGATA	
GAGATTATAT	CAGTGTCTGC	ATAACCATGA	GTGATAACAC	TGCGGCGCAAC	TTACTTCTGA	
CAACGATCCG	AGGACCGAAG	GAGCTAACCG	CTTTTTTGCA	CAACATGGGG	GATCATGTAA	
CTCGCTTGA	TCGTTGGGAA	CCGGAGCTGA	ATGAAGCCAT	ACCAAACGAC	GAGCGTGACA	
CCACGATGCC	TGTAGCAATG	GCAACAACGT	TGCGCAAACT	ATTAACCTGGC	GAACACTCTTA	
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AGGAAGCAGA ACCTTACTAT TTGTCTGCCA CAGCCGCGCT GGCAGGGTTG CCCCTGCGTT
CCGCCTGGGC AATCGCTACG GCGAAGCAGG TTTACCGGAA AATAGGTGTC AAAGTTGAAC
AGGCCGGTCA GCAAGCCTGG GATCAGCGGC AGTCAACGAC CACGCCCGAA AAATTAAACGC
TGCTGCTGGC CGCCTCTGGT CAGGCCCTTA CTTCCCGGAT GCGGGCTCAT CCTCCCCGCC
CTGCGCATCT CTGGCAGCGC CCGCTCTAGC GCCATGTCGA CCTCGAGGGG GGGCCCGGTA
CCCAATTGCG CCTATAGTGA GTCGTATTAC GCGCGCTCAC TGGCCGTGCT TTTACACGT
CGTGACTGGG AAAACCTTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC
GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC
CTGAATGGCG AATGGAAATT GTAAGCGTTA ATATTTTGT TAAAATTCGCG TTAATTTTT
GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAATCAA
AAGAATAGAC CGAGATAGGG TTGAGTGTG TTCCAGTTTG GAACAAGAGT CCACTATTAA
AGAACGTGGA CTCCAACGTC AAGGGCGGAA AACCGTCTA TCAGGGCGAT GGCCCACTAC
GTGAACCATC ACCCTAATCA AGTTTTTTGG GGTGAGGGT CCGTAAAGCA CTAATCGGA
ACCTTAAAGG GAGCCCCGA TTTAGAGCTT GACGGGGAAA GCGGCGGAAC GTGGCGAGAA
AGGAAGGGAA GAAAGCGAAA GGAGCGGGC CTAGGGCGCT GGCAAGTGTA GCGGTACACG
TGCGCGTAAC CACCACACC GCCGCGCTTA ATGCGCGCT ACAGGGCGCG TCAG

//

Annex F

DNA sequence of the vector construct pACYCcaro14

ID PACYCCARO14 PRELIMINARY; DNA; 8547 BP.
 SEQ SEQUENCE 8547 BP; 1884 A; 2296 C; 2279 G; 2088 T; 0 OTHER;

GAATTCGCGA TGAGCATTCA TCAGGCGGGC AAGAATGTGA ATAAAGGCCG GATAAAACTT
 GTGCTTATTT TTCCTTACGG TCTTTAAAAA GGCCGTAAATA TCCAGCTGAA CGGCTGTGGT
 ATAGGTACAT GTGACAACTG ACTGAAATGC CTCAAAATGT TCTTTACGAT GCCATTGGGA
 TATATCAACG GTGGTATATC CAGTGATTTT TTCTCCATT TTAGCTTCCT TAGCTCCTGA
 AAATCTCGAT AACTCAAAAA ATACGCCCGG TAGTGATCTT ATTTCATTAT GGTGAAAGTT
 GGAAGCTCTT ACGTGCCGAT CAACGTCTCA TTTTCGCCAA AAGTTGGCCC AGGGCTTCCC
 GGTATCAACA GGGACACCGA GATTATTATTA TTCTGCGAAG TGATCTTCGG TCACAGGTAT
 TTATTCGGCG CAAAGTGCCT CGGGTGATGC TGCCCACTTA CTGATTTAGT GTATGATGTT
 GTTTTGTAGG TGCTCCAGTG GCTTCTGTTT CTATCAGCTG TCCCTCCTGT TCAGCTACTG
 ACGGGGTGGT GCGTAAACCG AAAAGCACCG CCGGACATCA GCGTAGCGG AGTGATATACT
 GGCTTACTAT GTTGGCACTG ATGAGGGTGT CAGTGAAGTG CTTCATGTGG CAGGAGAAAA
 AAGGCTGCAC CGGTGCGTCA GCAGAATATG TGATACAGGA TATATTCCGC TTCTCGCTC
 ACTGACTCGC TACGCTCGGT CGTTCGACTG CGGCGAGCGG AAATGGCTTA CGAACGGGGC
 GGAGATTTCG TGGAAGATGC CAGGAAGATA CTTAACAGGG AAGTGAGAGG GCCCGGCGAA
 AGCCGTTTTT CCATAGSCTC GCCCCCCTG ACAAGCATCA CGAAATCTGA CGCTCAAACT
 AGTGTGTGGC AAAACCGACA GCACTATAAA GATACAGGC GTTTCGCCCT GCGCGCTCCC
 TCGTGCCTC TCCGTGCTCT GCCTTTCGTT TTACCGGTGT CATTCGCTG TTATGGCCGC
 GTTTGTCTCA TTCCACGCGT GACACTCAGT TCCGGGTAGG CAGTTCGCTC CAACTGTGAC
 TGATGTCACG AACCCCCGT TCAGTCCGAC CGTGCCTGCT TATCCGGTAA CTATCGTCTT
 GAGTCCAACC CGGAAGACA TGCAAAAGCA CCACTGGCAG CAGCCACTGG TAAATTGATT
 AGAGGAGTTA GTCTTGAAAT CATGCGCCGG TTAAGGCTAA ACTGAAAGGA CAAAGTTTGG
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 ATTTATCTCT TCAAAATGTAG CACCTGAAGT CAGCCCATTA CGATATAAGT TGTAATTCTC
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 AACGCAGTCA GGCACCGGTG ATGAAATCTA ACAATGCGCT CATCGTCAT CTGCGACCG
 TCACGCTGGA TCGTGTAGG ATAGGCTTGG TTATGCCGCT ACTGCCGGGC CTCCTGCGG
 ATATCGTCCA TTCCGACAGC ATCGCCAGTC ACTATGGCGT GCTGTAGCG CTATATGCGT
 TGATGCAATT CGTATGCGCA CCGCTTCTCG GAGCACTGTC CGACCGCTTT GCGCCCGCGC
 CAGTCTGCTC TCGTTGCTA CTTGGAGCCA TATCGACTA CGCGATCATC GCGACACAC
 CGGTCTGTG GATCCCCCGG GCTGCAGGAA TTGCGGTAAA TGATTCGGT TATAGGACA
 GCCCGAATGA CGGTCTGCGC AAAAACAAC GTTCATCTCA CTCGCGATG CTGCGGACAG
 TTAATGCGCT ATATTGATCG ACGCCTTGAT CAGTTATTGC CCGTGGAGGG AGAACGGGAT
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 TTGCTGTGTC TGACCGCCCG CGATCTGGGT TGCGCTGTCA GCCATGACGG ATTAATGGAT
 TTGGCCTGTG CCGTGGAAAT GGTCCACGCG GCTTCGCTGA TCTTTCAGCA TATGCCCTGC
 ATGGACGATG CGAAGCTGCG GCGCGGACGC CTAACCATC ATTCTCATTA CGGAGAGCAT
 GTGGCAATAC TGCGCGCGGT TGCCCTTGCT AGTAAGGCTT TTGGCGTAA TCGCGATGCG
 GATGCGCTCA GCGCGCTGGC AAAAATACGG GCGGTTTCTG AACTGTCAAA CGCCATCGCA
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 GCTGAAGCTA TTTTGATGAC GAATCACTTT AAAACGACGA CGCTGTTTGT TGCTCCATG
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 ACCGTGAAG ATAGCAATCA GGACGCGGTT AAATCGACGC TGGTCAATCT GTTAGGCGCG
 AGGGCGGTG AAGAAGCTCT GAGACAACAT CTTAGCTTGC CAGTGAGCA TCTCTCTGG
 GCCTGCCAAC ACGGGCACGC CACTCAACAT TTTATTGAG CTTGGTTTGA CAAAAAATC
 GCTGCGGTCA TTAAAGCTTA TGTGCAACCG TGAGCTGTG TTAAGTGCGGA CGGCTATG
 AACCCGATTA TGATCTGATT CTCGTGGGGG CTGGACTCGC GAATGGCCCT ATCGCCCTGC

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GTAAGCTGAA CAGCGGCTAC TTTTGATTA TTCTTCAGC TTTTCGTAG GTTTTCACAG
GACAGTTTGG CCCGCACTTG TGGATGGATA CCGCGGTCCG AGAGGTTAAT GTTTTACAGT
TTCCGTTGAA AAAGGGTCAG GTTATCGGTG CCCGCGCGGT GATTGACGGG CGGGGTTATG
CGCAAAATTC AGCACTGAGC GTGGGCTTCC AGGCGTTTAT TGGCCAGGAA TGGCGATTGA
GCCAACCCGA TGGTTTATCG TCTCCCATTA TCATGGATGC CACGGTTCGAT GAGCAAAATG
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ACTATATTGA TAAATGCGACA TTAGATCCTG AATGCGCGCG GCAAAATATT TGCAGCTATG
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TGTGGTTTAT ACCTATCGCG ACCTGTTAAG CCAGCACCCCT CGCGCGGTTA AGCAGTCCAA
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CGCCATTGCG ACGATGTTAT TCAGCATCAG ACGTGGGCT TTCAGGCCCG CGACGCTGCC
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CGCGCACCTG AAAACCGTCA GGCCTGTAGC CGTATGGCCC GTCTTGTGGT GCAGGAAGCA
GAACCTTACT ATTTGTCTGC CACAGCCGGC CTGGCAGGTT TGCCCTTGGC TTCCGCTTGG

GCAATCGCTA CGGCGAAGCA GGTTTACCGG AAAATAGGTG TCAAAAGTTGA ACAGGCCGGT
CAGCAAGCCT GGGATCAGCG GCAGTCAACG ACCACGCCCG AAAAATTAAC GCTGCTGCTG
GCCGCTCTG GTCAGGCCCT TACTTCCCGG ATGCGGGCTC ATCCTCCCGG CCCTGCGCAT
CTCTGGCAGC GCCCGCTCTA GCGCCATGTC GACCGATGCC CTTGAGAGCC TTCAACCCAG
TCAGCTCCTT CCGGTGGGCG CGGGGCATGA CTATCGTCGC CGCACTTATG ACTGTTCTCT
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TCGCGGCTCT TACCAGCCTA ACTTCGATCA CTGGACCGCT GATCGTCACG GCGATTATG
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TCTGCTCCCC CGCGTTGCGT CGCGGTGCAT GGAGCCGGGC CACCTCGACC TGAATTGGAAG
CCGGCGGCAC CTCGTAACG GATTACCCAC TCCAGAATT GGAGCCATC AATTCTTGCG
GAGAATCTGT AATGCGCAAA CCAACCCTTG GCAGAACATA TCCATGCGT CCGCATCTCT
CAGCAGCCGC ACGCGCGCA TCTCGGGCAG CGTTGGGTCC TGGCCACGGG TGCGCATGAT
CGTGCTCCTG TCGTTGAGGA CCCGGCTAGG CTGGCGGGGT TGCCTTACTG GTTAGCAGAA
TGAATCACCG ATACCGGAGC GAACGTGAAG CGACTGCTCG TGCAAAACGT CTGGACACTG
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TATGACTGTC TTCTTTATCA TGCAACTCGT AGGACAGGTG CCGGCAGCGC CCAACAGTCC
CCCGCCACG GGGCCTGCCA CCATACCCAC GCCGAAACAA GCGCCTGTCA CCATTATGTT
CCGGATCTGC ATCGCAGGAT GCTGCTGGCT ACCCTGTGGA ACACCTACAT CTGTATTAAAC
GAAGCGCTAA CCGTTTTTAT CAGGCTCTGG GAGGCAGAAT AAATGATCAT ATCGTCAATT
ATTACCTCCA CGGGAGAGC CTGAGCAAAC TGGCCTCAGG CATTTGAGAA GCACACGGTC
ACACTGCTTC CGGTAGTCAA TAAACCGGTA AACACGCAAT AGACATAAGC GGCTATTTAA
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GCTTATTATC ACTTATTCAG CGGTAGCACC AGGCGTTTAA GGGCACC AAT AACTGCTTTA
AAAAAATTAC GCCCCGCCCT GCCACTCATC GCAGTACTGT TGAATTATCAT TAAGCATTTCT
CCGACATAG AAGCCATCAC AGACGGCATG ATGAACCTGA ATCGCCAGCG GCATCAGCAC
CTTGTGCGCT TGCGTATAAT ATTTGCCCAT GGTGAAAACG GGGCGAAGA AGTTGTCCAT
ATTGGCCACG TTTAAATCAA AACTGGTGAA ACTCACCCAG GGATTGGCTG AGACGAAAAA
CATATTCTCA ATAAACCTTT TAGGGAAATA GGCCAGGTTT TCACCGTAAC ACGCCACATC
TTGCGAATAT ATGTGTAGAA ACTGCCGAA ATCGTCGTGG TATTCATCTC AGAGCGATGA
AAACGTTTCA GTTTGCTCAT GGAACACCGT GTAACAAGGG TGAACACTAT CCCATATCAC
CAGCTCACCG TCTTTATCTG CCATACG

Annex G

DNA and corresponding amino acid sequence of the *ispG* (formerly *gcpE*) gene of*Escherichia coli*

10	20	30	40	50	60
ATGCATAACCAAGGCTCCAATTCAACGTAGAAAATCAACACGTATTACGTTGGGAATGTG					
M H N Q A P I Q R R K S T R I Y V G N V					
70	80	90	100	110	120
CCGATTGGCGATGGTGCTCCCATCGCCGTACAGTCCATGACCAATACGCGTACGACAGAC					
P I G D G A P I A V Q S M T N T R T T D					
130	140	150	160	170	180
GTGCAAGCAACGGTCAATCAAATCAAGCGCTGGAACGCGTTGGCGCTGATATCGTCCGT					
V E A T V N Q I K A L E R V G A D I V R					
190	200	210	220	230	240
GTATCCGTACCGACGATGGACGCGGAGCAAGCGTTCAAACATCAAAACAGCAGGTTAAC					
V S V P T M D A A E A F K L I K Q Q V N					
250	260	270	280	290	300
GTGCCGCTGGTGCTGACATCCACTTCGACTATCGCATTGGCGCTGAAAGTAGCGGAATAC					
V P L V A D I H F D Y R I A L K V A E Y					
310	320	330	340	350	360
GGCGTCGATTGTCTGCGTATTAACCCCTGGCAATATCGGTAATGAAGAGCGTATTGCGATG					
G V D C L R I N P G N I G N E E R I R M					
370	380	390	400	410	420
GTGGTTGACTGTGCGCGGATAAAAACATTCCGATCCGTTATTGGCGTTAACGCGGATCG					
V V D C A R D K N I P I R I G V N A G S					
430	440	450	460	470	480
CTGGAAAAAGATCTGCAAGAAAAGTATGGCGAACCGACGCCGAGCGTTGCTGGAATCT					
L E K D L Q E K Y G E P T P Q A L L E S					
490	500	510	520	530	540
GCCATGCGTCATGTTGATCATCTCGATCGCCTGAACCTTGATCAGTTCAAAGTCAGCGTG					
A M R H V D H L D R L N F D Q F K V S V					

550 560 570 580 590 600
| | | | | |
AAAGCGTCTGACGTCTTCTCGCTGTTGAGTCTTAICGTTTGCTGGCAAACAGATCGAT
K A S D V F L A V E S Y R L L A K Q I D

610 620 630 640 650 660
| | | | | |
CAGCGGTTGCATCTGGGGATCACCGAAGCCGGTGGTGGCGCAGCGGGGCAGTAAATCC
Q P L H L G I T E A G G A R S G A V K S

670 680 690 700 710 720
| | | | | |
GCCATTGGTTTAGGTCTGCTGCTGTCTGAAGGCATCGCGACACGCTGCGCGTATCGCTG
A I G L G L L L S E G I G D T L R V S L

730 740 750 760 770 780
| | | | | |
GCGCGCATCCGGTCGAAGAGATCAAAGTCGGTTTCGATATTTGAAATCGCTGCGTATC
A A D P V E E I K V G F D I L K S L R I

790 800 810 820 830 840
| | | | | |
CGTTCGCGAGGGATCAACTTCATCGCCTGCCCGACCTGTTTCGCGTCAGGAATTGATGTT
R S R G I N F I A C P T C S R Q E F D V

850 860 870 880 890 900
| | | | | |
ATCGGTACGGTTAAACGCGCTGGAGCAACGCCTGGAAGATATCATCACTCCGATGGACGTT
I G T V N A L E Q R L E D I I T P M D V

910 920 930 940 950 960
| | | | | |
TCGATTATCGGCTGCGTGGTGAATGGCCAGGTGAGGCGCTGGTTTCTACACTCGGCGTC
S I I G C V V N G P G E A L V S T L G V

970 980 990 1000 1010 1020
| | | | | |
ACCGGCGGCAACAAGAAAAGCGGCCTCTATGAAGATGGCGTGGCGCAAGACCGTCTGGAC
T G G N K K S G L Y E D G V R K D R L D

1030 1040 1050 1060 1070 1080
| | | | | |
ARCAACGATATGATCGACCAGCTGGAAGCACGCATTCGTGCGAAAGCCAGTCAGCTGGAC
N N D M I D Q L E A R I R A K A S Q L D

1090 1100 1110
| | |
GAAGCGGTCGAATTGACGTTTACGAGGTTGAAAAATAA
E A R R I D V Q Q V E K -

Annex H

DNA sequence of the vector construct pBScyclogcpE

ID	BSBSCYLOG	PRELIMINARY;	DNA;	8823 BP.			
5Q	SEQUENCE	8823 BP;	2123 A;	2169 C;	2468 G;	2063 T;	0 OTHER;
	GTGGCACTTT	TCGGGGAAAT	GTGCGCGGAA	CCCTATTTTG	TTTATTTTTC	TAAATACATT	
	CAAAATATGTA	TCCGCTCATG	AGACAAATAC	CCTGATAAAT	GCCTCAATAA	TATTGAAAAA	
	GGAGAGCATAT	GAGTATATCAA	CATTTCCTGT	TGCGCCCTTT	TCCTCTTTTT	CGCGGCATTT	
	GCCTTCCTGT	TTTGTGCTAC	CCAGAAAGTG	TGGTGAAAGT	AAAAGATGCT	GAAATACAGT	
	TGGGTGCGCAG	AGGTGGGTTAT	ATGCAACTGT	ATCTCAACAG	CGGTAAAGAT	CTTTGAGAGT	
	TTGCGCCGCA	AGAACTGTTT	CCAAATGATG	GCACTTTTAA	AGTTCTGTCTA	TGTGGCGCGG	
	TATTATCCCG	TATTGACGCC	GGGCAAGAGC	AACTCGGTG	CCGCATACAC	TATTCTCAGA	
	ATGACTTGGT	TGAGTACTCA	CCAGCTACAG	AAAAGCATCT	TACGAGTGGC	ATGACAGTAA	
	GAGAATTATG	CAGTGTGCGC	ATAAGTCAAT	GTGATAACAC	TGCGGCCAAC	TACTTCTTGT	
	CAACGATCGG	AGGACCGAAG	GAGCTAACCG	CTTTTGTGCA	CACATCGGGG	GATCATGTGA	
	TCGCGCTTGA	CTGTGGGAA	CGGGAGCTGA	ATGAAGCCAT	ACCACACGAC	GAGCGTGACA	
	CCACGATGCC	TGTAGCAATG	GCAACAACGT	TGCGCAAAC	ATTAACCTGGC	GAACTACTTA	
	CTCTAGCTTC	CCGGCAACAA	TTAATAGACT	GGATGGAGGC	GGATAAAGTT	CGGAGGACAC	
	TTCTCGCTCC	GGCCCTTCCG	GCTGGCTGGT	TATTGTCTGA	TAAATCTGGA	GCGCGTAGGC	
	TGTGGGTCTG	CGGTATCATC	CGCAGCATGG	GGCCAGATGG	TAAAGCCCTCC	CGTATCGGTA	
	TATTCTACAC	GACGGGGAGT	CAGGCAACCTA	TGGATGAACG	AAAATAGACG	ATCGCTGAGT	
	TAGGTGCCTC	ACTGATTAA	CATTGGTAA	TGTGACAGCA	AGTTTACTCA	TATATACTTT	
	AGATTGATTT	AAAACTTCT	TTTAAATTTA	AAAGGATCTA	GGTGAAGATC	CTTTTGTGTA	
	ATCTCATGAC	CAAAATCCAT	TAACTGTAGT	TTTGTCTTCA	CTGAGCGTCA	GACCCCGTAG	
	AAAAAGTCAA	AGGATCTTCT	TGAGATCTTT	TTTTTCTGCG	CGTAATCTGC	TGCTTGCCTAA	
	CAAAAAAAC	ACCGCTACCA	CGGGTGGTTT	GTTTTCCGGA	TCGAAAGATTA	CCAACTCTTA	
	TTCCGAAGGT	AACGTGCTTC	AGCAGAGCGC	AGATATCCAA	GTATTCCTTT	CTAGTGTAGC	
	CGTAGTTAGG	CCACCACTTC	AGAACACTGT	TAGCACCGCC	TACATACCTC	CTCTGCTGTA	
	TCCTGTTACC	AGTGGCTGCT	GCCAGTGGCG	ATAAGTCGTG	TCTTACCCGG	TTGGAATCAA	
	GACGATAGTT	AGCGGATAAG	GCGCAGCGGT	CGGGCTGAAC	GGGGGGTTG	TGCACACAGC	
	CAGAGCTTGA	GCGAAGCAGC	TACACCAAGC	TGAGATACT	ACAGCGTCCG	CTATGACAGC	
	CCGCGACGCT	TCCGGAAGGG	AGAAAGAGCG	ACAGATATCC	GGTAAGCGGC	AGGGTCGGAA	
	CAGGAGAGCG	CACGAGGAG	CTTCACGGGG	GAAATCGCTG	GTATCTTTAT	AGTCTGCTCG	
	GGTTTCGCAA	CCCTGACTTT	GAGCGTCAT	TTTGTGATG	CTCTGCAGGG	GGGCGGAGCC	
	TATGAAAAAA	CGCCACGAA	CGCGGCTTTT	TACGGTTCCT	GGCCTTTTTC	TGGCCCTTTG	
	CTACCATGTT	CTTTCTCGG	TATTCCTGCT	ATTCTGTGTA	TAAACGTTAT	ACCGCCTTTG	
	AGTGAAGCTG	TACCGCTCGC	CGCAGCGGAA	CGCAGCGAGC	GACCGAGTCA	TGTGAGCGAG	
	AAGCGGAAGA	GCGCCAAAT	CGCAAAACGC	CTCTCCCCGC	CGGTTGGCCG	ATTATCAATG	
	TGAGTGTGCA	CGACAGCTTT	CCGACTGAGA	AGGCGGGCAG	TGAGCGCAAC	GCAATTAAATG	
	CGACTTAGCT	CATCTATTAG	GACCCCAAG	CTTTACACTT	TATGCTTCCG	GCTCGTATGT	
	TGTTGTGAAT	TGTGAGCGGA	TAAACAATTC	ACACAGAGAA	CAGCATGATG	CATGATATAG	
	CCAAAGCGCG	AATTAACCTC	CACCTAAAGCT	ACAAAGAGCT	GGAGCTCCAC	CGCGGGAGAG	
	GAAATTAAC	ATGCTATAAC	AGGCTTCAAT	TCAAGTAAAT	AAGATAACAC	GTAITTAAGT	
	TGGGAATATG	CGGATGGCG	ATGGTGTCTC	CATCGCGGTA	GCTGCCATGA	CCAAATACGG	
	TACGACAGAC	TGTCGAAGCA	CGGTCAATTA	ATACAGGGC	CTGGAAACGC	TTGGCGCTTA	
	TATCTGTCGT	GTATCCGTAC	CGACGATGGA	CGCGGCAGAA	CGGTTCAAAC	TCATCAAACA	
	GCAGGTTAAC	GCGGCTCGTG	TGGCTGATCA	CCACTCTGAC	TATGCTATTG	CGTGAAGAT	
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CGGTACAGCT CCGCGTAACC ACCACACCG CCGCGCTTAA TGCGCCGCTA CAGGGCGCGT
CAG

Annex I

DNA sequence of the vectorconstruct pACYClytBgcpe

ID PACYCGCLY PRELIMINARY; DNA; 5793 BP.
 SQ SEQUENCE 5793 BP; 1375 A; 1506 C; 1543 G; 1369 T; 0 OTHER;

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Annex J

A and corresponding amino acid sequence of the *ispH* (formerly *lytB*) gene from *Escherichia coli*

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M Q I L L A N P R G F C A G V D R A I S I V E N

      80      90      100     110     120     130     140
GCGCTGGCAATTACGGCGCACCGATATATGTCCTGACGAAGTGATACATAACCGCTATGTTGGTCATAGC
A L A I Y G A P I Y' V R H E V V H N R Y V V D S

      150     160     170     180     190     200     210
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L R E R G A I F I E Q I S E V P D G A I L I F S

      220     230     240     250     260     270     280
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A H G V S Q A V R N E A K S R D L T V F D A T C

      290     300     310     320     330     340     350     360
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P L V T K V H M E V A R A S R R G E E S I L I G

      370     380     390     400     410     420     430
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H A G H P E V E G T M G Q Y S N P E G G M Y L V

      440     450     460     470     480     490     500
GAATCGCCGGACGATGTGTGGAACCTGACGGTCAAAAACGAAGAGAAGCTCTCCTTTATGACCCAGACCAAG
E S P D D V W K L T V K N E E K L S F M T Q T T

      510     520     530     540     550     560     570
CTGTGCGTGGATGACAGTCTGATGTGATCGACGCGCTGCGTAAACGCTTCCGAAAATTGTCGGTCCGCGC
L S V D D T S D V I D A L R K R F P K I V G P R

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K D D I C Y A T T N R Q E A V R A L A E Q A E V

      650     660     670     680     690     700     710     720
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V L V V G S K N S S H S N R L A E L A Q R M G K

      730     740     750     760     770     780     790
CGCGGTTTTTGATTGACGATGCGAAGACATCCAGGAAGAGTGGGTGAAGAGGTTAAATGCTGCGCGTG
R A F L I D D A K D I Q E E W V K E V K C V G V

      800     810     820     830     840     850     860
ACTGCGGCGCATCGGCTCCGATATTCTGTGTCAGAAATGKTTGGCAOGTTTGACGACGCTGGGCGGTGT
T A G A S A P D I L V Q N V V A R L Q Q L G G G

      870     880     890     900     910     920     930

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940 950
CGTGAAGTCGATTAA
R E V D -

Annex K

DNA Sequence of the plasmid construct pBSscyllogcpElytB2

ID PBSXICH2 PRELIMINARY; DNA; 9795 BP.

SEQUENCE 9795 BP; 2351 A; 2401 C; 2770 G; 2273 T; 0 OTHER;

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AGATTGATTT AAAACTTCAT TTTTAAATTA AAAGGATCTA GGTGAAGATC CTTTTTGATA
ATCTCATGAC CAAAAATCCCT TAACGTGAGT TTTGCTTCCA CTGAGCGTCA GACCCCGTAG
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CAAAAACAAAC ACCGCTACCA CGCGTGGTTT GTTTGCCGGA TCAAGAGCTA CCAACTCTTT
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TCCTGTTACC AGTGGCTGCT GCCAGTGGCG ATAAGTCTGT TCTTACCGGG TTGAGACTCA
GACGATAGTT ACCGGATAAG GCGCAGCGGT CGGCTGAAC GGGGGGTTTC GTGACACAGC
CCAGCTTGGG GCGAACGACC TACACCGAAC TGAGATACCT ACAGCGTGAG CTATGAGAAA
GCGCCACGCT TCCCGAAGGG AGAAAGCGGG ACAGGTATCC GGTAGCGGCG AGGGTCTGGAA
CAGGAGAGCG CACGAGGGAG CTTCAGGGGG GAAACGCCTG GTATCTTTAT AGTCCTGTGC
GGTTTCGCGA CCTTGACTT GAGCGTGCAT TTTTGTGATG CTGTCGACGG GGGCGGAGCC
TATGAAAAAA CGCCAGCAAC GCGGCCCTTT TACGGTTCCT GGCCCTTTTC TGGCCTTTTG
CTCAGATGTT CTTTCTGCG TTATCCCTG ATTTCTGTGA TAACCGTATT ACCCGCTTTG
AGTGAAGTGA TACCGCTCGC GCGAGCGGAA CGACCGGAGC CAGCGAGTGA GTGAGCGAGG
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TGAGTTAGCT CACTCATTAG GCACCCCAAG CTTTACACTT TATGCTTCGG GCTCGTATGT
TGTGTGGAAT TGTGAGCGGA TAACAATTTC ACACAGGAAA CAGCTATGAC CATGATTACG
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TGGGAATGTT CGGATTGGCG ATGGTGCTCC CATCGCCGTA CAGTCCATGA CCAATACGCG
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TATCGTCCGT GTATCCGTAC CGACGATGGA CGCGGACGAA GCGTTCARAC TCTCAACAA
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CGCGGATATG CTGGAATAAG ATCTGCAAGA AAGTATGTCG GAACGACGCG CACAGCGCTT
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CTACAGCAAC AGGGTAGCCG CACCGAAGTC TTAAGTGGGC AACAGCCGCG TTGCGATATG

GCAGCGCTTG AGGATGTTGA TCAGGTGATG GCAGCCATTG TTGGCGCTGC TGGGCTGTTA
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CATGCGCTCG TGGCGCATCC CGGCGTGAA CGTGTCTGCA TTGCCATAAG TCCTGGCGAT
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TGCCGCGACAT TCCACAAATG CGCGTGTGTTA TTGCCGAAGA TCTCGGCTGC CATATGGATG
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TTGCCCTGTGA AGCGGTGGCG CTACTCAITA AGGCAACAAA ATGACTCTGAG GAGGAGAATG
TAACACTCGG GACACAGTGG CCGCTCTCGG CAAAAATCTAA TCTGTTTTTA TACATTAACG
GTCAGCGTGC GGATGGTTAC CACACGCTGC AAACGCTGTT TCAGTTTCTT GATTACGGCG
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ATCATCTCTG GCAATGCGGG CTAAGCATGG ATGAGCTGCG GGAATGGGG CTGACGCTGG
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TTCCGAACTCC GGTGATTTTT AAAGATCTCG AACTCCCGCG CAATACGCCA AAAAGGTCAA
TAGAAAAGTT GCTAAAATGT GAATTCAGCA ATGATTGCGA GTTATCGCA AGAAAACGTT
TTGCGGAGGT TGATGCGGTG CTTTCTGGC TGTAGAATA CGCCCGCTCG CAGCTGACTG
GGACAGGGCG CTGTGTCTTT CACTGAATTTG ATACAGATC TGAAGCCCGC CGCTGCTAG
AGCAAGCCCC GGAATGGCTC AATGGCTTTG TGGCGAAAGG CGCTAATCTT TCCCATTTG
ACAGAGCCAT GCTTTAAGGT ACCCAATTCG CCTATAGTG AGTCGTATTA CGCGCGCTCA
CTGGCGCTCG TTTTACAAAG TCGTGACTGG GAAAACCTCG CGGTACCCA ACTTAATGCT
CTTGCAAGCAC ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATTCG
CTTCTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGAAAT TGTAAAGCCTT AATATTTTGT
TAAATTCGCG GTTAAATTTT TGTAAATCA GCTCATTTTT TAACCAATAG GCGGAAATCG

GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG GTTGAGTGTT GTTCAGTTT
GGAACAAGAG TCCACTATTA AAGAACGTGG ACTCCAACGT CAAAGGGCGA AAAACCGTCT
ATCAGGGCGA TGGCCCACTA CGTGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT
GCCGTAARAG ACTAAATCGG AACCCCTAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC GCTAGGGCGC
TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC CGCCGCGCTT AATGCGCCGC
TACAGGGCGC GTCAG

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Annex L

DNA and corresponding amino acid sequence of the *ispG* gene (fragment) from*Arabidopsis thaliana*

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      10      20      30      40      50      60      70
>AAGACGGTGAGAGGAAGACTCGTACTGTTATGGTTGGAATGTCGCCCTTGGAGGCGAACATCCGATAAGG
  K T V R R K T R T V M V G N V A L G S E H P I R

      80      90      100     110     120     130     140
ATTCAAAGCATGACTACTTCGGATACAAAGATATTACTGGAACCTGGATGAGGTTATGAGAAATAGCGGAT
  I Q T M T T S D T K D I T G T V D E V M R I A D

     150     160     170     180     190     200     210
AAAGGAGCTGATATTGTAAGGATAACTGTTCAAGGGAAGAAAGGCGGATGCGTGCTTTGAAATAAAGAT
  K G A D I V R I T V Q G K K E A D A C F E I K D

     220     230     240     250     260     270     280
AAACTCGTTCAGCTTAATTACAATACACGCTGTTGCAAGTATTCAITTTGCCCTACTGTAGCCTTAGCA
  K L V Q L N Y N T F L V A G I H F A P T V A L R

     290     300     310     320     330     340     350     360
GTCCGCTGAATGCTTTGACAAGATCCGTGTCAACCCCGGAAATTTGCGGACAGGCGGGCCAGTTTGAGAGC
  V A E C F D K I R V N P G N F A D R R A Q P E T

     370     380     390     400     410     420     430
ATAGATTATACAGAAGATGAATATCAGAAAGAACTCCAGCATATCGAGCAGGTCTTCACTCCTTTGGTTGAG
  I D Y T E D E Y Q K E L Q H I E Q V F T P L V E

     440     450     460     470     480     490     500
AAATCGAAGAGTACGGGAGAGCAATGCGTATTGGGACAAATCATGGAAGTCTTTCTGACGGTATCATGAGC
  K C K K Y G R A M R I G T N H G S L S D R I M S

     510     520     530     540     550     560     570
TATTACGGGGATCTCCCGAGGAATGGTTGAATCTGCGTTGAGTTTGCAAGAATATGCGGAATTAGAC
  Y Y G D S P R G M V E S A F E F A R I C R K L D

     580     590     600     610     620     630     640
TATCACAACTTTGTTTTCTCAATGAAGCGAGCAACCCAGTGATCATGGTCCAGGCGTACCGTTTACTGTG
  Y H N F V F S M K A S N P V I M V Q A Y R L L V

     650     660     670     680     690     700     710     720
GCTGAGATGATCTTCATGGATGGGATATCCCTTTCAGTTGGGAGTTACTGAGGCAGGAGAGGGCGAAGAT
  A E M Y V H G W D Y P L H L G V T E A G E G E D

     730     740     750     760     770     780     790
GGACCGATGAATCTGCGATTGGAATTGGGACGCTTCTTCAGGACGGGCTCGGTGACACACAGAGATTCA
  G R M K S A I G I G T L L Q D G L G D T T R V S

     800     810     820     830     840     850     860
CTGACGGAGCCACCAGAAGAGGAGATAGATCCCTGACGGCGATTGGCTAACCTCGGGACAAAGCTGCCAAA

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L T E P P E E E I D P C R R L A N L G T K A A K
 870 880 890 900 910 920 930
 CTTCAACAAGGCGCTGCACCGTTTGAAGAAAAGCATAGGCATTACTTTGATTTTCAGCGTCGGACGGGTGAT
 L Q Q G A A P F E E K H R H Y F D F Q R R T G D
 940 950 960 970 980 990 1000
 CTACCTGTACAAAAGAGGGAGAAAGGTTGATTACAGAAATGCTCTCACCGTGATGGTCTGTTCTGATG
 L P V Q K E G E E V D Y R N V L H R D G S V L M
 1010 1020 1030 1040 1050 1060 1070 1080
 TCGATTTCCTGGATCAACTAAGGGCACCTGAACTCTCTACAGATCACTCGCCACAAGCTTGTCTGGGT
 S I S L D Q L K A P E L L Y R S L A T K L V V G
 1090 1100 1110 1120 1130 1140 1150
 ATGCCATTCAAGGATCTGGCACTGTGATTCAATCTTATTAAAGAGCTACCGCTGTAGATGATCAAGTG
 M P F K K D L A T V D S I L L R E L P P V D D Q V
 1160 1170 1180 1190 1200 1210 1220
 GCTCGTTGGCTCTCAACCGGTTGATGATGTCAGTATGGAGTTATAGCACCTTTATCAGAGCAACTAACA
 A R L A L K R R L I D V S M G V I A P L S E Q L T
 1230 1240 1250 1260 1270 1280 1290
 AAGCCATTGCCAATGCCATGGTCTCTGTCACTCAAGGAATCACTGGTGGCGCTTACAAGCTTCTCCCT
 K P L P N A M V L V N L K E L S G G A Y K L L P
 1300 1310 1320 1330 1340 1350 1360
 GAAGGTACAGCTTGGTTGTCTCTCTACGAGGCGATGAGCCTTACGAGGAGCTTGAAATACTCAAAAACATT
 E G T R L V V S L R G D E P Y E R L E I L K N I
 1370 1380 1390 1400 1410 1420 1430 1440
 GATGCTACTATGATCTCCATGATGTACCTTCTACTGAAGACAAAGTTAGCAGAGTACATCGAGCTCGGAGG
 D A T M I L H D V P F T E D K V S R V H A A R R
 1450 1460 1470 1480 1490 1500 1510
 CTATTGAGTCTTATCCGAGAATTCACTTAACCTTCTGTTAATCATGCATAAACTCCCAACCGGAATC
 L P E F L S E N S V N F P V I H R I N F P T G I
 1520 1530 1540 1550 1560 1570 1580
 CACAGAGACGAATTGGTGATTCATGACGGGACATATGCTGGAGGCCCTCTTGTGGATGGACTAGGTGATGC
 H R D E L V I H A G T Y A G G L L V D G L G D G
 1590 1600 1610 1620 1630 1640 1650
 GTAATGCTCGAAGCACCTGACCAAGATTTTGATTTCTTAGGAATCTTCTTCAACTTATTACAAAGGATGC
 V N L E A P D Q D F D F L R N T S F N L L Q G C
 1660 1670 1680 1690 1700 1710 1720
 AGAATGCGTAACACTAAGACGGATATGTATCTGTCGCCGCTCTGTGGAGAAGCGCTTTTCGACTGCAAGAA
 R M R N T K T E Y V S C P S C G R T L F D L Q E
 1730 1740 1750 1760 1770 1780 1790 1800
 ATCAGCGCCGAGATCCGAGAAAAGACTTCCCACTTACCTGGCGCTTCGATCGCAATCATGGGATGCATTGTG
 I S A E I R E K T S H L P G V S I A I M G C I V
 1810 1820 1830 1840 1850 1860 1870

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      |           |           |           |           |           |
AATGACCAGGAGAAATGGCAGATGCTGATTTCGGATATGTAGGTGGTTCTCCCGGAAAAATCGACCTTTAT
N G P G E M A D A D F G Y V G G S P G K I D L Y

      1880      1890      1900      1910      1920      1930      1940
      |           |           |           |           |           |
GTCGAAAGACGGTGGTGAAGCGTGGGATAGCTATGACGGAGGCCAACAGATGCTCTGATCGGTCTGATCAAA
V G K T V V K R G I A M T E A T D A L I G L I K

      1950      1960      1970      1980
      |           |           |           |
GAACATGGTCGTTGGGTCGACCGCCCGTGGCTGATGAGTAG
E H G R W V D F P V A D E -

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Annex M
DNA and corresponding amino acid sequence of the *ispG* (formly *gcpE*) gene of
Arabidopsis thaliana

ATGGCGACTGGAGTATTGCCAGCTCCGGTTTCTGGGATCAAGATACCGGATTGCGAAAGTC	60
M A T G V L P A P V S G I K I P D S K V	20
GGGTTTGGTAAAGCATGAATCTTGTGAGAATTTGTGATGTTAGGAGTCTAAGATCTGCT	120
G F G K S M N L V R I C D V R S L R S A	40
AGGAGAAGAGTTTCGGTTATCCGGAATCAAACCAAGGCTCTGATTAGCTGAGCTTCAA	180
R R R V S V I R N S N Q G S D L A E L Q	60
CCTGCATCCGAAGGAAGCCCTCTCTTAGTGCCAAGACAGAAATATTGTGAATCATTGCAT	240
P A S E G S P L L V P R Q K Y C E S L H	80
AAGACGGTGAGAAGGAAGACTCGTACTGTTATGGTTGGAATGTCGCCCTTGGGAAGCGAA	300
K T V R R K T R T V M V G N V A L G S E	100
CATCCGATAAGGATTCAAACGATGACTACTTCGGATACAAAGATATTACTGGAAGTGT	360
H P I R I Q T M T T S D T K D I T G T	120
GATGAGGTTATGAGAATAGCGGATAAAGGAGCTGATATTGTAAGGATAACTGTTCAAGGG	420
D E V M R I A D K G A D I V R I T V Q G	140
AAGAAAGAGGCGGATGCGTGCTTTGAAATAAAAGATAAACTCGTTCAGCTTAATTACAAT	480
K K E A D A C F E I K D K L V Q L N Y N	160
ACACCGCTGGTTGCAGGTATTCATTTTGCCTTACTGTAGCCTTACGAGTCGCTGAATGC	540
T P L V A G I H F A P T V A L R V A E C	180
TTTGACAAGATCCGTGTCAACCCCGGAAATTTTGGCGACAGGCGGGCCAGTTTGAGACG	600
F D K I R V N P G N F A D R R A Q F E T	200
ATAGATTATCAGAAGATGAATATCAGAAAGAACTCCAGCATATCGAGCAGGTCTTCACT	660
I D Y T E D E Y Q K E L Q H I E Q V F T	220
CCTTTGGTTGAGAAATGCAAAAAGTACGGGAGAGCAATGCGTATTGGGACAAATCATGGA	720
P L V E K C K K Y G R A M R I G T N H G	240
AGTCTTTCTGACCGTATCATGAGCTATTACGGGGGATTTCTCCCGAGGAATGGTTGAATCT	780
S L S D R I M S Y Y G D S P R G M V E S	260
GC GTTTAGTTTTCGAAGAATATGTCGGAAATTAGACTATCACAACTTTGTTTCTCAATG	840
A F E F A R I C R K L D Y H N F V F S M	280
AAAGCGAGCAACCCAGTGATCATGGTCCAGGCGTACCGTTTACTTGTGGCTGAGATGTAT	900
K A S N P V I M V Q A Y R L L V A E M Y	300
GTTTCATGGATGGGATTATCCTTTGCATTTGGGAGTTACTGAGGCAGGAGAAGCGAAGAT	960
V H G W D Y P L H L G V T E A G E G E D	320
GGACGGATGAAATCTGCGATTGGAATTGGGACGCTTCTTCAGGACGGGCTCGGTGACACA	1020

G R M K S A I G I G T L L Q D G L G D T

ACAAGAGTTTCACTGACGGAGCCACCAGAAGGAGATAGATCCCTGCAGGCGATTGGCT 1080
T R V S L T E P P E E E I D P C R R L A 360

AACCTCGGGACAAAAGCTGCCAACTTCAACAAGGCGCTGCACCGTTTGAAGAAAAGCAT 1140
N L G T K A A K L Q Q G A A P F E E K H 380

AGGCATTACTTTGATTTTCAGCGTCGGACGGGTGATCTACCTGTACAAAAAGAGGGAGAA 1200
R H Y F D F Q R R T G D L P V Q K E G E 400

GAGGTTGATTACAGAAATGTCTTCACCGTGATGGTTCTGTTCTGATGTCGATTCTCTG 1260
E V D Y R N V L H R D G S V L M S I S L 420

GATCAACTAAAGGCACCTGAACCTCTACAGATCACTCGCCACAAAGCTTGTCTGGGT 1320
D Q L K A P E L L Y R S L A T K L V V G 440

ATGCCATTCAAGGATCTGGCAACTGTTGATTCAATCTTATTAAGAGAGCTACCGCCTGTA 1380
M P F K D L A T V D S I L L R E L P P V 460

GATGATCAAGTGGCTCGTTTGGCTCTCAAACGGTTGATTGATGTCAGTATGGGAGTTATA 1440
D D Q V A R L A L K R L I D V S M G V I 480

GCACCTTTATCAGAGCAACTAACAAAGCCATTGCCAATGCCATGGTTCTTGTCACCTC 1500
A P L S E Q L T K P L P N A M V L V N L 500

AAGGAAGTATCTGTTGGCGCTTACAAGCTTCTCCCTGAAGGTACACGCTTGGTTGTCTCT 1560
K E L S G G A Y K L L P E G T R L V V S 520

CTACGAGGCGATGAGCCTTACGAGGAGCTTGAATACTCAAAAACATTGATGCTACTATG 1620
L R G D E P Y E E L E I L K N I D A T M 540

ATTCTCCATGATGTACCTTTCACTGAAGACAAAGTTAGCAGAGTACATGCAGCTCGGAGG 1680
I L H D V P P T E D K V S R V H A A R R 560

CTAITCGAGTTCTTATCCGAGAATTCAAGTTAACTTTCCTGTTATTCATCGCATAAACTTC 1740
L F E F L S E N S V N F P V I H R I N F 580

CCRACCGGAATCCACAGAGCGAATTGGTGATTTCATGCAGGGACATATGCTGGAGGCCCTT 1800
P T G I H R D E L V I H A G T Y A G G L 600

CTTGTGGATGAGCTAGGTGATGGCGTAATGCTCGAAGCACCTGACCAAGATTTTGAATTT 1860
L V D G L G D G V M L E A P D Q D F D F 620

CTTAGGAATACTTCTTCAACTTATTACAAGGATGCAGAAATGCGTAACACTAAGACGGAA 1920
L N T S F N L L Q G C R M R N T K T E 640

TATGTATCGTGCCGCTCTGTGGAAGAACGCTTTTCGACTTGCAAGAAATCAGCGCCGAG 1980
Y V S C P S C G R T L F D L Q E I S A E 660

ATCCGAGAAAAGACTTCCCATTTACCTGGCGTTTCGATCGCAATCATGGGATGCATTGTG 2040
I R E K T S H L P G V S I A I M G C I V 680

AATGGACCAGGAGAAATGGCAGATGCTGATTTTCGATATGTAGGTGTTCTCCCGGAAA 2100

N G P G E M A D A D F G Y V G G S P G K 700

ATCGACCTTTATGTCGGAAGACGGTGGTGAAGCGTGGGATAGCTATGACGGAGGCAACA 2160

I D L Y V G K T V V K R G I A M T E A T 720

GATGCTCTGATCGGTCTGATCAAAGAACATGGTCGTTGGGTCGACCCGCCGTGGCTGAT 2220

D A L I G L I K E H G R W V D P P V A D 740

GAGTAG 2226

E - 741

Annex N

cDNA sequence of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (IspH)

from *Arabidopsis thaliana*

ATGGCTGTTGCGCTCCAATTCAGCCGATTATGCGTTCGACCCGGATACCTTCGTGCGGGAGAATCATCTCTCT	72
M A V A L Q F S R L C V R P D T F V R E N H L S	24
GGATCCGGATCTCTCCGCGCCGGAAGCTTTATCAGTCCGGTGCTCGTCTGGCGATGAGAACGCTCCTTCG	144
G S G S L R R R R K A L S V R C S S S G D E N A P S	48
CCATCGGTGTTGATGGACTCCGATTCGACGCCAAGGTGTTCCGTAAGAACTTGACGAGAACGCGATAATTAC	216
P S V V M D S D F D A K V F R K N L T R S D N Y	72
AATCGTAAGGGTTTCGGTCATAAGGAGGAGACACTCAAGCTCATGAATCGAGATACACCAGTGATATATTG	288
N R K G F G H K E E T L K L M N R E Y T S D I L	96
GAGACACTGAAAACAAATGGGTATATCTTCTGGGAGATGTTACTGTGAACTCGCTAAAGCATATGGT	360
E T L K T N G Y T Y S W G D V T V K L A K A Y G	120
TTTTGCTGGGGTGTGAGCGTGCTGTTTCAGATTGCATATGAAGCAGCAAGCGTTCAGAGGAGAGGCGT	432
F C W G V E R A V Q I A Y E A R K Q F P E E R L	144
TGGATTACTAACGAAATCATTCATAACCCGACCGTCAATAAGAGGTTGGAAGATATGGATGTTAAATTAT	504
W I T N E I I H N P T V N K R L E D M D V K I I	168
CCGGTTGAGGATTCAGAAACAGTTTGATGTAGTAGAGAAAGATGATGTGGTTATCCTTCCTCGCTTTGGA	576
P V E D S K K Q F D V V E K D D V V I L P A F G	192
GCTGGTGTGACGAGATGTATCTTAAATGATAAAAGGTGCAAAATGTTGACACACTTGTCTCTGGGTG	648
A G V D E M Y V L N D K K V Q I V D T T C P W V	216
ACAAGGTCTGGAACACGCGTTGAGAAGCACAGAAGGGGAATACACATCAGTAATCCATGGTAAATATAAT	720
T K V W N T V E K H K K G E Y T S V I H G K Y N	240
CATGAAGAGACGATTGCAACTCGCTCTTTGACGAGAAAGTACATCATTGTAAGAAACATGAAGAGGCAAT	792
H E E T I A T A S F A G K Y I I V K N M K E A N	264
TACGTTGTGATTACATCTCGGTGGCCAATACGATGGATCTAGCTCCACAAAGAGAGGTTCFMGAGAAA	864
Y V C D Y I L G G Q Y D G S S S T K E E F M E K	288
TTCAAATACGCAATTTGGAAGGGTTTCGATCCCGACAATGACCTTGTCAGAGTTGGTATTGTCAAACCAACA	936
F K Y A I S K G F D P D N D L V K V G I A N Q T	312
ACGATGCTAAAGGGGAGAAACAGAGGAGATAGGAAGATTACTCGAGACAACATGATGCGCAAGTATGGAGTG	1008
T M L K G E T E E I G R L L E T T M M R L S N T S H	336
GAAATGTAAAGCGGACATTTTCATCAGCTTCAACACAATATGCGACGCTACTCAAGAGCGACAAGACGCAATC	1080
E N V S G H F I S F N T I C D A T Q E R Q D A I	360
TATGAGCTAGTGAAGAGAAATTGACCTCATGCTAGTGGTTGGCGGATGGAATCAAGTAACACCTCTCAC	1152
Y E L V E L K E I D L M L V V G G W N S N C T S H	384
CTTCAGGAAATCTCAGAGGCACGGGAATCCCATCTTACTGGATCGATAGTGAGAAACGGATAGGACCTGGG	1224
L Q E I S E A R G I P S Y W I D S E K R I G P G	408
AATAAATAGCCTATAAGCTCCACTATGGAGAACTGGTCGAGAAGGAAACCTTCTCCCAAGGGACCAATA	1296
N K I A Y K L H Y G E L V E K E N F L P K G P I	432
ACAATCGGTGTGATCAGGTGCATCAACCCGGGATAAGGTCGTGGAAGATGCTTTGGTGAAGGTGTTTCGAC	1368
T I G V T S G A S T P D K V V E D A L V K V F D	456
ATTAAACGTGAAGAGTTATTGCACTGGCTTGA	1398
I K R E E L L Q L A -	466